

## FIGURE 1

### MOUSE B7x PROTEIN SEQUENCE

MASLGQIIFWSIINIILLAGAIALIIGFGISGKHFITVTTFTSAGNIGEDGTLSCTFEPDIKLNQIVIQWL  
KEGIKGLVHEFKEGKDDLSSQHEMFRGRTAVFADQVVVGNASLRLKNVQLTDAGTYTCYIRTS  
KGKGNANLEYKTGAFSMPEINVDYNASSESLRCEAPRWFPQPTVAWASQVDQGANFSEVSNT  
SFELNSENVTMKVSVLYNVTINNTYSCMIENDIAKATGDIKVTDSSEVKRRSQLQLLNSGPSPCV  
FSSAFAAGWALLSLSCCLMLR

### HUMAN B7x PROTEIN SEQUENCE

MASLGQILFWSIISIIILLAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLSDIVIQWLKEG  
VLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGTYKCYIITSKGKGNANL  
EYKTGAFSMPEVNVYNASSETLRCEAPRWFPQPTVWASQVDQGANFSEVSNTSFELNSENVTM  
KVVSVLYNVTINNTYSCMIENDIAKATGDIKVTSEIKRRSHLQLLNSKASLCVSSFFAISWALLPLSPYL  
MLK

## FIGURE 2

### MOUSE B7x NUCLEIC ACID SEQUENCE

ATGGCTTCCTTGGGGCAGATCATCTTTTGGAGTATTATTAACATCATCATCATCCTGGCTGGGGC  
CATCGCACTCATCATTGGCTTTGGCATTTCAGGCAAGCACTTCATCACGGTCACGACCTTCACCT  
CAGCTGGAAACATTGGAGAGGACGGGACCCTGAGCTGCACTTTTGAACCTGACATCAAACCTCAA  
CGGCATCGTCATCCAGTGGCTGAAAGAAGGCATCAAAGGTTTGGTCCACGAGTTCAAAGAAGGC  
AAAGACGACCTCTCACAGCAGCATGAGATGTTGAGAGGCCGCACAGCAGTGTTTGCTGATCAGG  
TGGTAGTTGGCAATGCTTCCCTGAGACTGAAAAACGTGCAGCTCACGGATGCTGGCACCTACAC  
ATGTTACATCCGCACCTCAAAGGCAAAGGGAATGCAAACCTAGAGTATAAGACCGGAGCCTTC  
AGTATGCCAGAGATAAATGTGGACTATAATGCCAGTTCAGAGAGTTTACGCTGCGAGGCTCCTC  
GGTGGTTCCCCCAGCCCACAGTGGCCTGGGCATCTCAAGTCGACCAAGGAGCCAACTTCTCAG  
AAGTCTCGAACACCAGCTTTGAGTTGAACTCTGAGAATGTGACCATGAAGGTCGTATCTGTGCTC  
TACAATGTCACAATCAACAACACATACTCCTGTATGATTGAAAATGACATTGCCAAAGCCACTGG  
GGACATCAAAGTGACAGATTCAGAGGTCAAAGGCGGAGTCAGCTGCAGCTGCTCAACTCCGG  
GCCTTCCCCGTGTGTTTTTCTTCTGCCTTTGCGGCTGGCTGGGCGCTCCTATCTCTCTCCTGTT  
GCCTGATGCTAAGATGA

### FIGURE 3

#### HUMAN B7x NUCLEIC ACID SEQUENCE

ATGGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGC  
AATTGCACTCATCATTGGCTTTGGTATTTAGGGAGACACTCCATCACAGTCACTACTGTGCGCT  
CAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAAACCTTCT  
GATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCAAAGAAGGCAA  
AGATGAGCTGTGCGGAGCAGGATGAAATGTTGAGAGCCGGACAGCAGTGTTTGCTGATCAAGTG  
ATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATG  
TTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCA  
TGCGGGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATG  
GTTCCCCCAGCCCACAGTGGTCTGGGCATCCCAAGTTGACCAGGGAGCCAACCTTCTCGGAAGTC  
TCCAATACCAGCTTTGAGCTGAACTCTGAGAATGTGACCATGAAGGTTGTGTCTGTGCTCTACAA  
TGTTACGATCAACAACACATACTCCTGTATGATTGAAAATGACATTGCCAAAGCAACAGGGGATA  
TCAAAGTGACAGAATCGGAGATCAAAAGGCGGAGTCACCTACAGCTGCTAAACTCAAAGGCTTC  
TCTGTGTGTCTCTTCTTTCTTTGCCATCAGCTGGGCACTTCTGCCTCTCAGCCCTTACCTGATGCT  
AAAATAA

## FIGURE 4

[illegible]

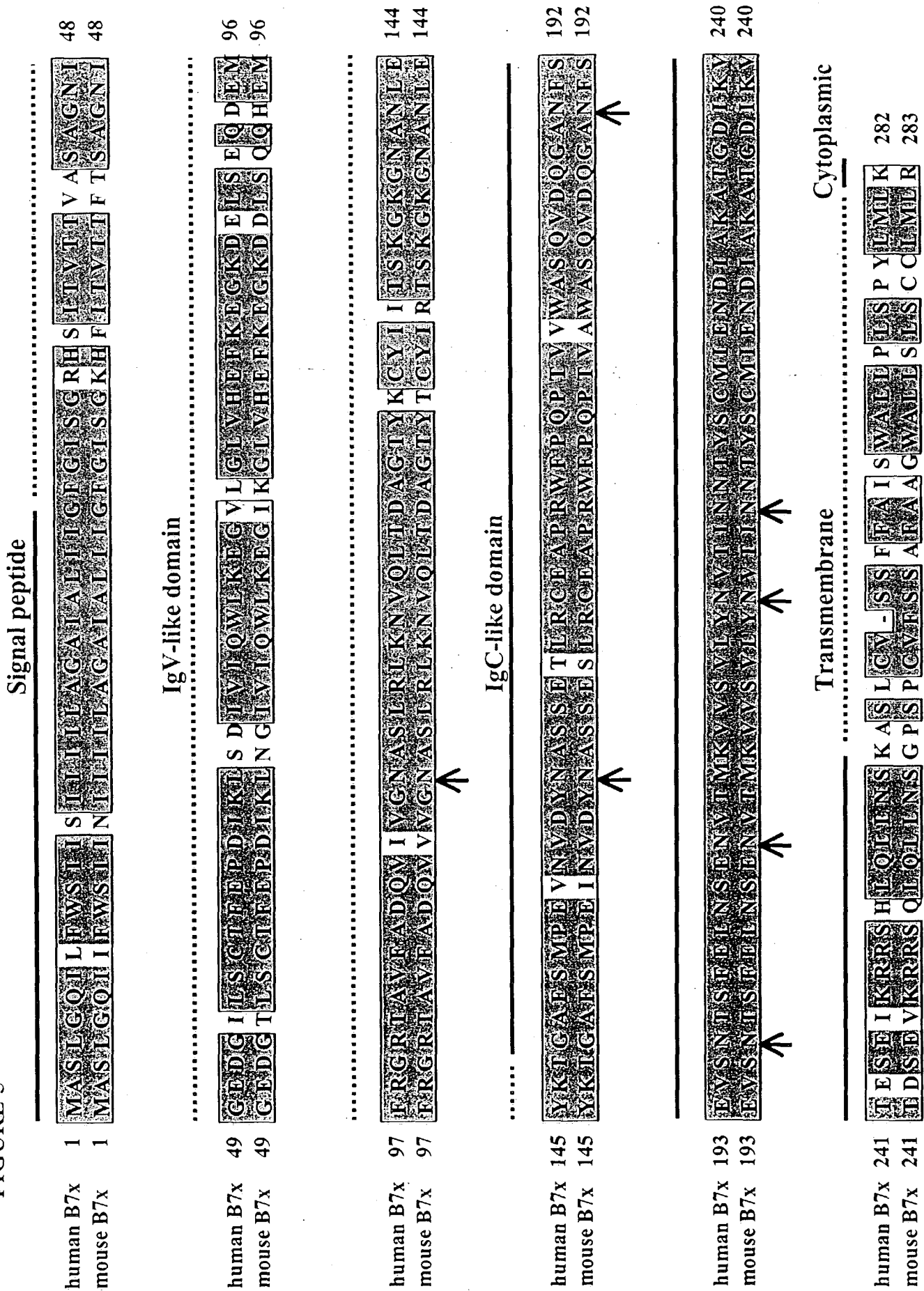
B7x	65	NGI	V	Q	W	R	E	G	-	-	-	I	K	G	L	V	H	E	F	K	E	G	K	D	I	L	S	Q	Q	H	E	M	F	R	G	R	T	A	V	F	A	D	Q	V	V	V	G	N	A	S	U	R	I	K	N	V	Q	L	T	D	A	G	T	Y	T	C	I	I	R	T	134	
B7.1	64	SED	R	I	Y	W	O	K	H	D	-	-	-	-	K	V	V	L	S	V	I	A	G	K	L	K	Y	W	P	E	Y	K	N	-	-	R	T	L	Y	D	N	T	T	-	-	-	-	S	L	I	I	L	G	L	V	L	S	D	R	G	T	S	V	W	Q	K	123					
B7.2	51	SEI	V	V	F	W	O	D	Q	Q	-	-	-	-	I	K	L	V	L	Y	E	H	Y	L	G	-	T	E	K	L	D	S	V	N	-	-	A	K	Y	T	G	R	T	S	F	D	R	N	N	W	T	U	R	I	K	N	V	Q	L	K	D	M	G	S	I	D	G	F	I	Q	K	114
B7h	73	SGI	Y	V	Y	W	O	I	E	N	P	E	S	V	T	Y	L	P	Y	K	S	P	G	-	I	N	V	D	S	S	Y	K	N	-	-	R	G	H	E	S	L	D	S	M	K	Q	G	N	F	S	L	Y	L	K	N	V	T	P	Q	D	T	O	E	F	T	G	R	V	F	M	142	
PD-L1	51	LAL	V	V	Y	W	E	R	E	D	-	-	-	-	E	Q	V	J	I	Q	F	V	A	C	E	-	D	L	K	P	Q	H	S	N	F	R	G	R	A	S	L	P	K	D	Q	L	K	G	N	A	L	Q	I	T	D	Y	V	C	I	I	S	Y	118									
PD-L2	53	EGI	R	A	S	L	O	K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	V	E	N	-	D	T	S	L	Q	-	S	E	-	-	R	A	T	L	E	E	Q	L	P	L	G	K	A	L	F	H	I	P	S	V	Q	V	R	D	S	Q	O	X	R	G	L	V	I	C	106
B7-2H3	61	AOL	N	L	I	W	O	L	T	D	-	-	-	-	T	K	Q	L	V	H	S	F	T	E	G	R	-	D	O	G	S	A	Y	S	N	-	-	R	T	A	L	F	P	D	L	V	Q	G	N	A	S	U	R	I	K	N	V	Q	L	T	D	E	G	S	Y	T	C	I	I	R	T	126

B7x	135	SKGK	---	---	GNAN	LEYK	GTGA	FSMP	---	---	EIN	VDYN	ASS	---	ESLR	CEAP	PRWF	QPTV	AWAS	QVDQ	GANF	SE	193		
B7.1	124	KERG	TYE	VKHL	ALV	KLSIK	ADFF	ST	---	---	PNIT	ESGN	PS	ADTK	RITC	FA	SGFP	PPRFS	SWLE	NGRE	---	LP	187		
B7.2	115	KPPT	GSI	ILQ	OTL	TES	SVIA	NFSE	P	---	---	EIKL	QNV	TG	NSGI	NJTG	TSKQ	GHPP	KKMY	FLIT	NS	TNEY	181		
B7h	143	NTAT	---	---	ELV	KIIL	EEV	RLR	VAA	NFST	PV	IST	SDSN	PG	Q	ERTY	TCMS	KN	CYPP	EPNL	YWIN	TTD	NSLI	210	
PD-L1	119	GQA	---	---	DYK	RIT	LKN	NA	PYRK	---	---	INQR	ISVD	PA	TSHE	HL	QA	-	EGYP	EAEW	IWT	NSD	HQ	176	
PD-L2	107	GAAW	---	---	DYK	YL	TVK	KAS	YMR	---	---	IDTR	LEV	PG	TGEV	QLTG	QA	-	RGYP	LAEM	SWQN	---	VSV	160	
B7-H3	127	QDF	---	---	DSA	AV	STQ	VAA	PYSKP	---	SMT	LEPN	KDL	LRPN	-	MVT	IF	SS	YQ	GYP	EAEM	FWK	DGQ	GV	188

194	B7x	V	S	N	T	S	F	E	L	N	S	E	N	V	T	M	K	V	V	S	V	L	N	V	T	I	--	N	N	T	S	S	C	M	I	E	N	D	I	--	A	K	A	T	G	D	J	K	V	T	D	S	E	V	K	R	R	S	--	Q	L	Q	L	N	S	C	--	257					
188	B7.1	I	N	T	I	S	Q	D	P	E	S	E	T	Y	T	I	S	S	O	T	D	N	T	R	--	N	H	T	I	K	C	L	I	K	Y	G	D	--	A	H	V	S	E	D	F	T	W	E	K	P	P	E	D	P	P	D	S	K	N	T	I	V	L	F	C	A	G	F	255				
182	B7.2	D	N	M	Q	I	S	Q	B	N	V	T	E	T	F	S	I	S	N	S	I	S	F	P	D	G	V	H	M	T	V	V	C	V	L	E	T	E	S	--	M	K	J	S	S	K	P	L	N	F	T	O	E	F	F	S	--	P	Q	T	V	W	K	E	I	T	A	S	V	250			
211	B7h	L	Q	N	T	V	Y	L	N	K	L	G	T	Y	D	V	I	S	T	L	R	L	P	W	T	S	--	R	G	D	V	I	C	C	V	E	N	V	A	L	H	O	N	I	T	S	I	S	Q	A	E	S	F	T	G	N	N	T	K	N	P	Q	E	T	H	N	N	E	L	K	V	L	281
177	PD-L1	K	R	S	V	T	T	S	R	T	E	G	M	L	N	V	T	S	S	I	R	V	N	A	J	A	--	N	D	V	F	Y	C	T	F	W	R	S	Q	P	C	O	N	H	T	A	E	L	I	I	P	E	L	P	A	T	H	P	Q	N	R	T	H	W	V	L	L	G	S	I	L	247	
161	PD-L2	P	A	N	T	S	H	I	R	T	P	E	C	T	Y	Q	N	T	S	V	E	R	L	K	P	Q	P	--	S	R	N	F	S	C	M	F	W	N	A	H	--	M	K	E	L	T	S	A	I	I	D	P	L	S	R	M	E	P	K	Y	P	R	T	-	W	P	L	H	--	224			
189	B7-H3	N	V	T	S	Q	M	A	N	E	R	G	C	F	D	M	H	S	V	E	R	V	V	L	G	A	--	N	C	T	Y	S	C	L	V	R	N	P	V	L	Q	Q	D	A	H	G	S	V	T	I	T	G	Q	P	L	T	F	P	P	E	A	L	W	V	T	V	C	--	L	S	256		

[illegible]

FIGURE 5



## FIGURE 6

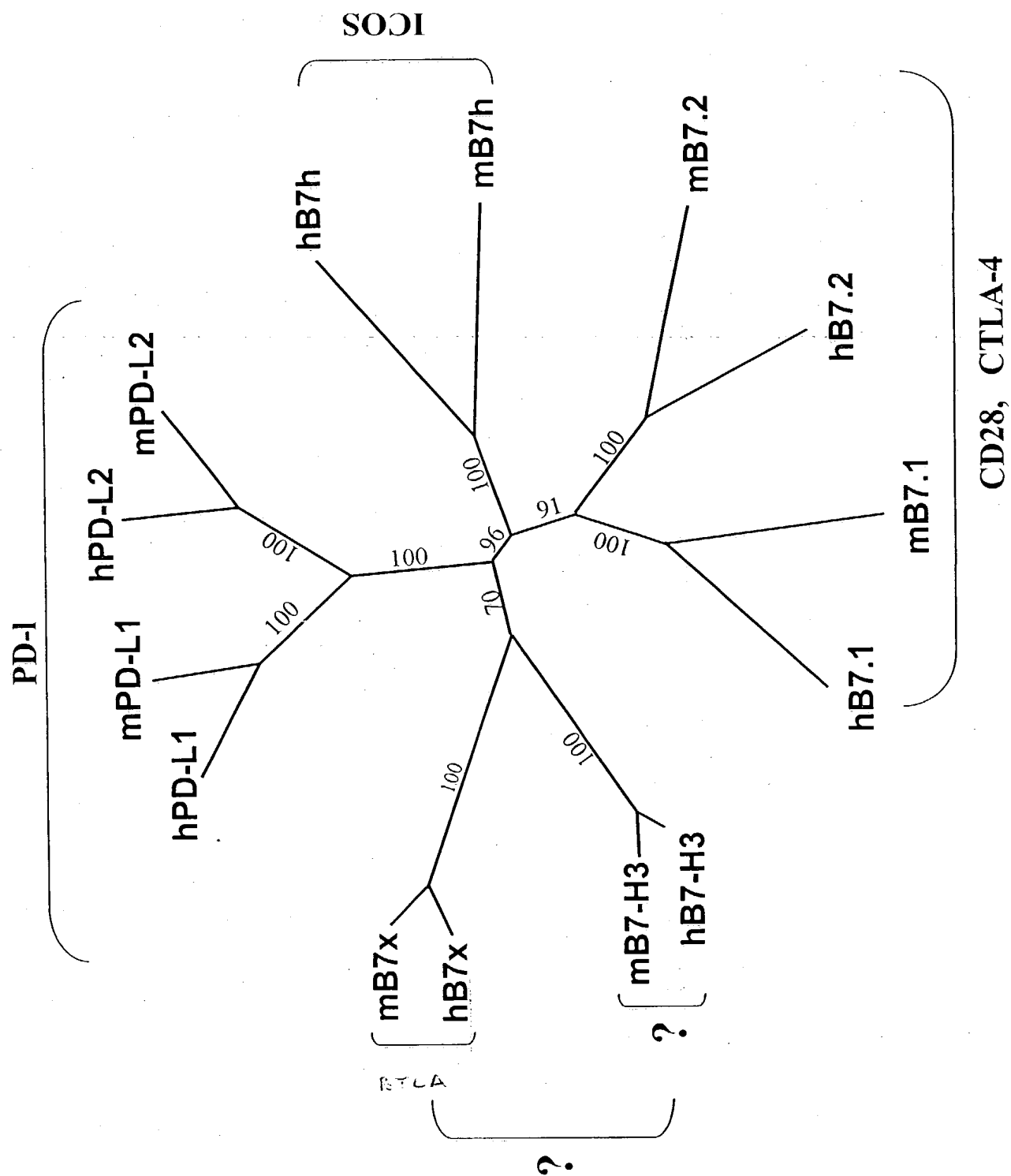


FIGURE 7

# Human

# Murine

PBL  
Lung  
Placenta  
Small intestine  
Liver  
Kidney  
Spleen  
Thymus  
Colon  
Skeletal muscle  
Heart  
Brain

Testis  
Kidney  
Skeletal muscle  
Liver  
Lung  
Spleen  
Brain  
Heart

9.5 —  
7.5 —  
4.4 —  
2.4 —  
1.35 —  
0.24 —

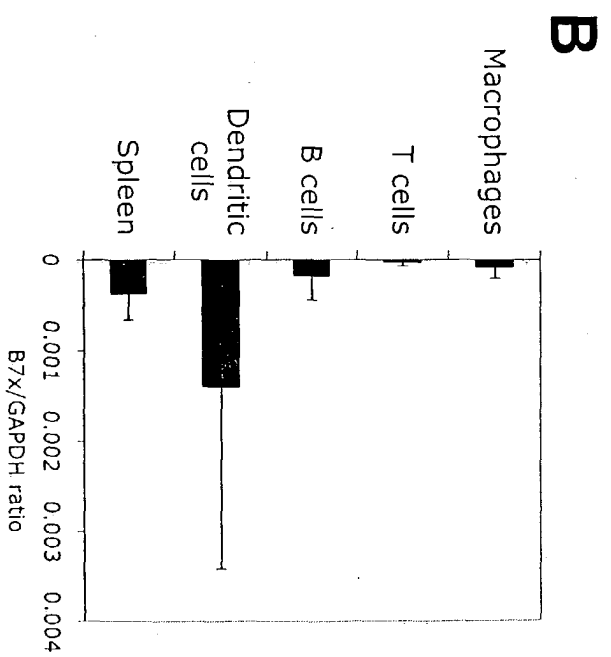
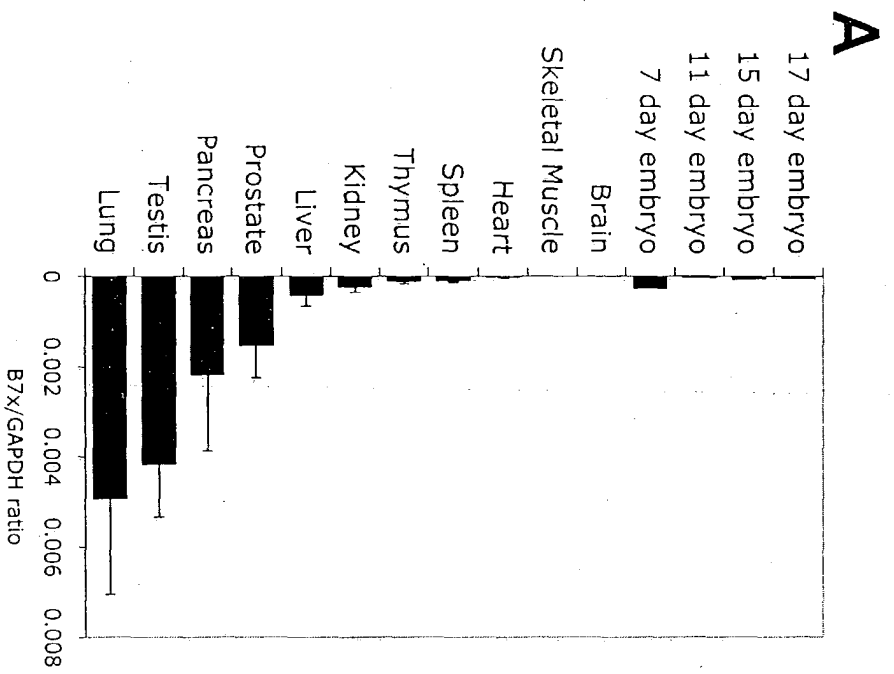
9.5 —  
7.5 —  
4.4 —  
2.4 —  
1.35 —  
0.24 —



B7x



Actin



**FIGURE 8**



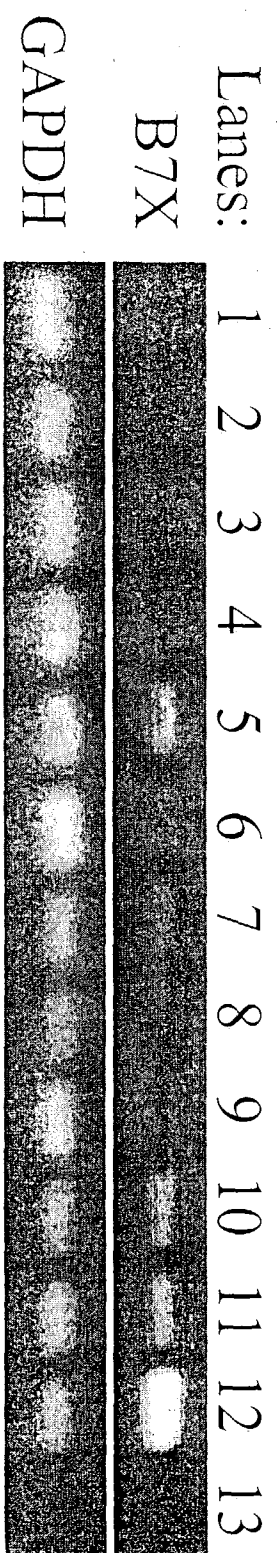


FIGURE 9

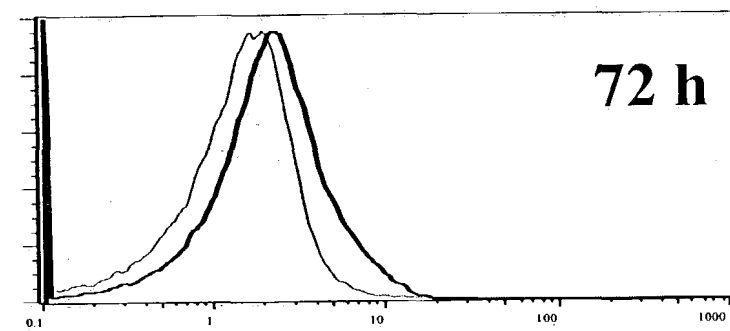
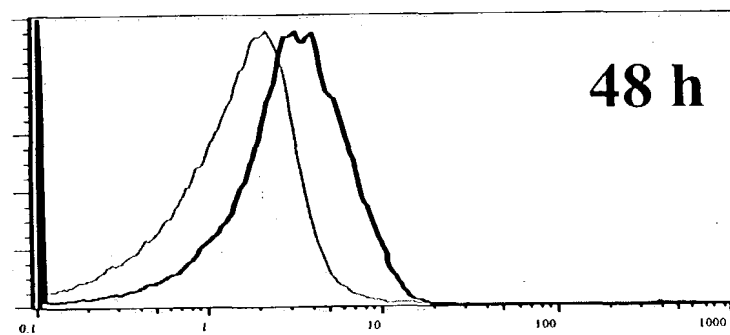
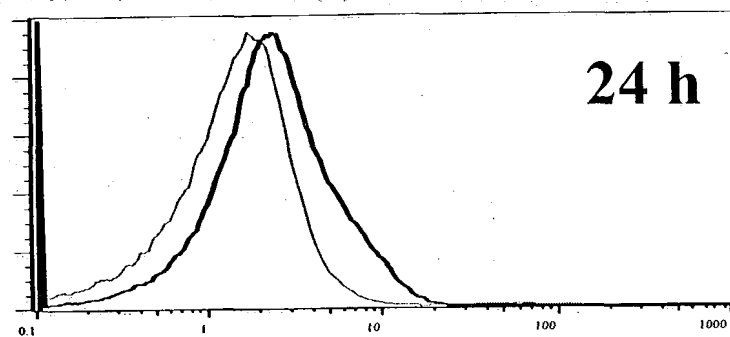
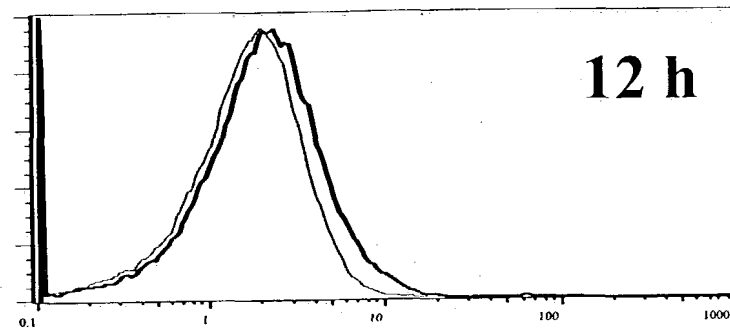
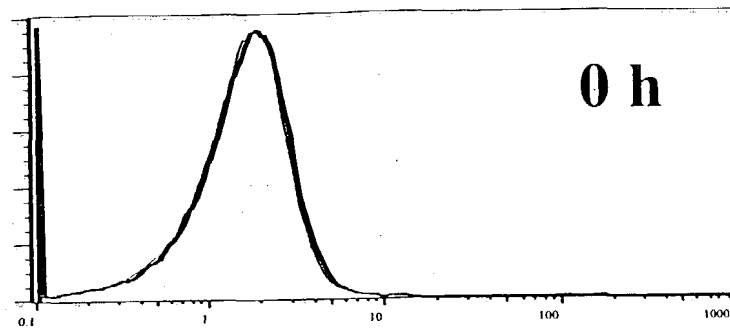
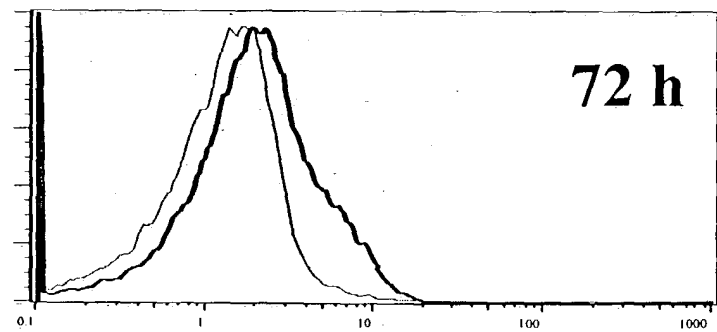
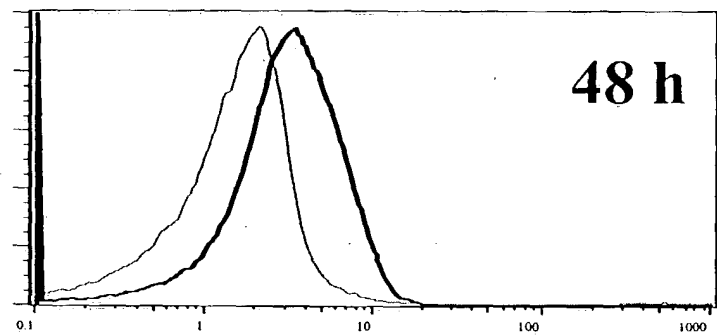
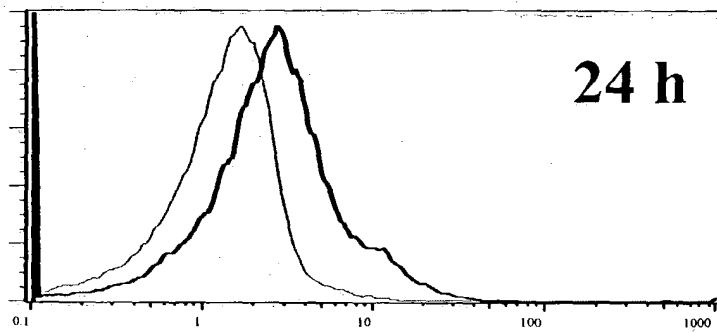
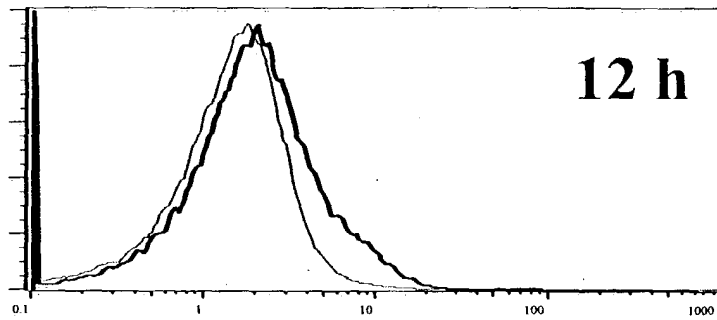
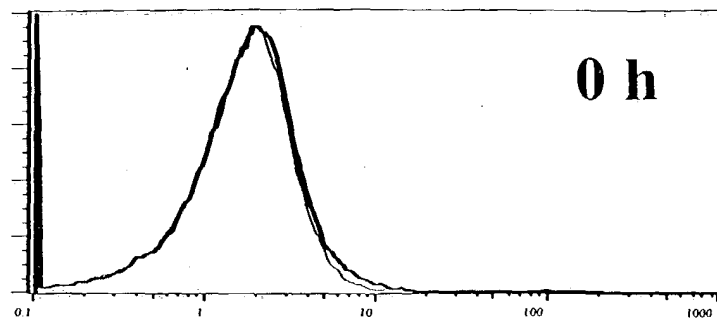
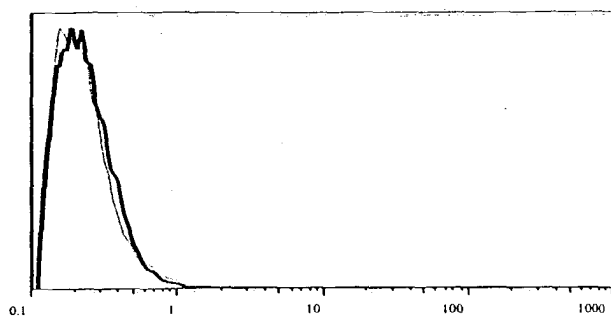


FIGURE 10

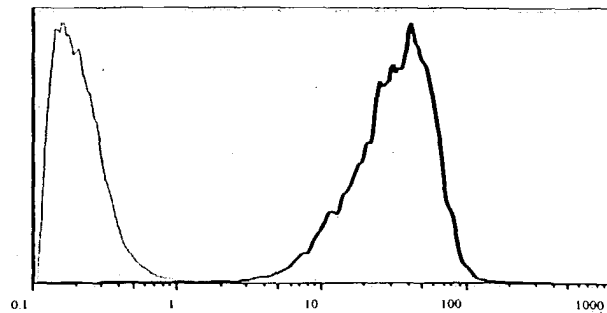


**FIGURE 11**

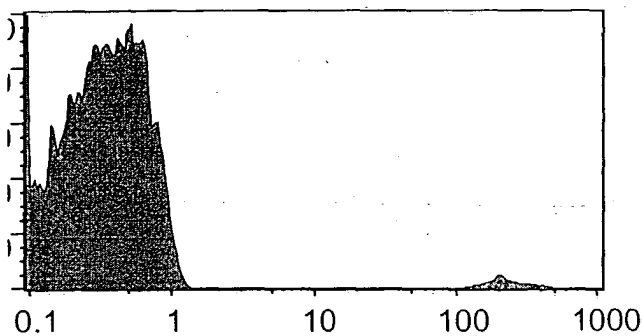
FIGURE 12



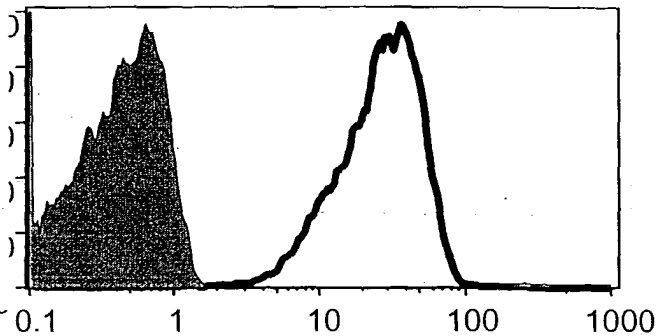
**B7x-Ig**



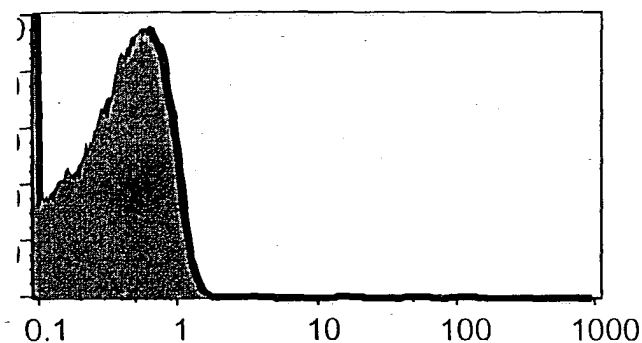
**Anti-CD28**



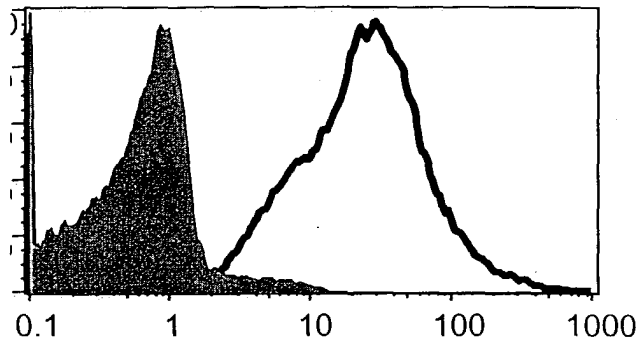
**B7x-Ig**



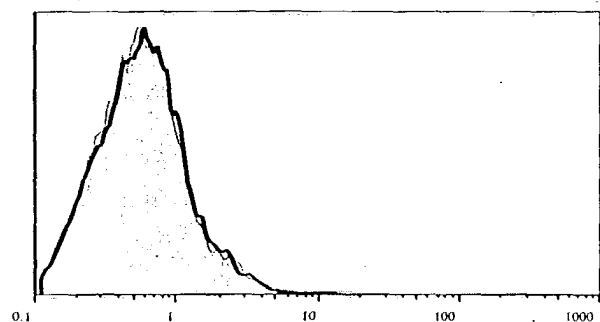
**Anti-ICOS**



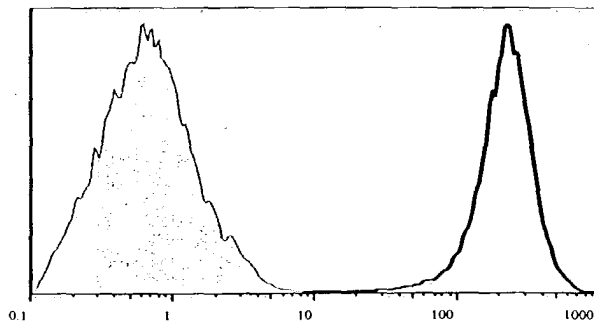
**B7x-Ig**



**Anti-PD-1**



**B7x-Ig**



**Anti-CTLA-4**

FIGURE 13A

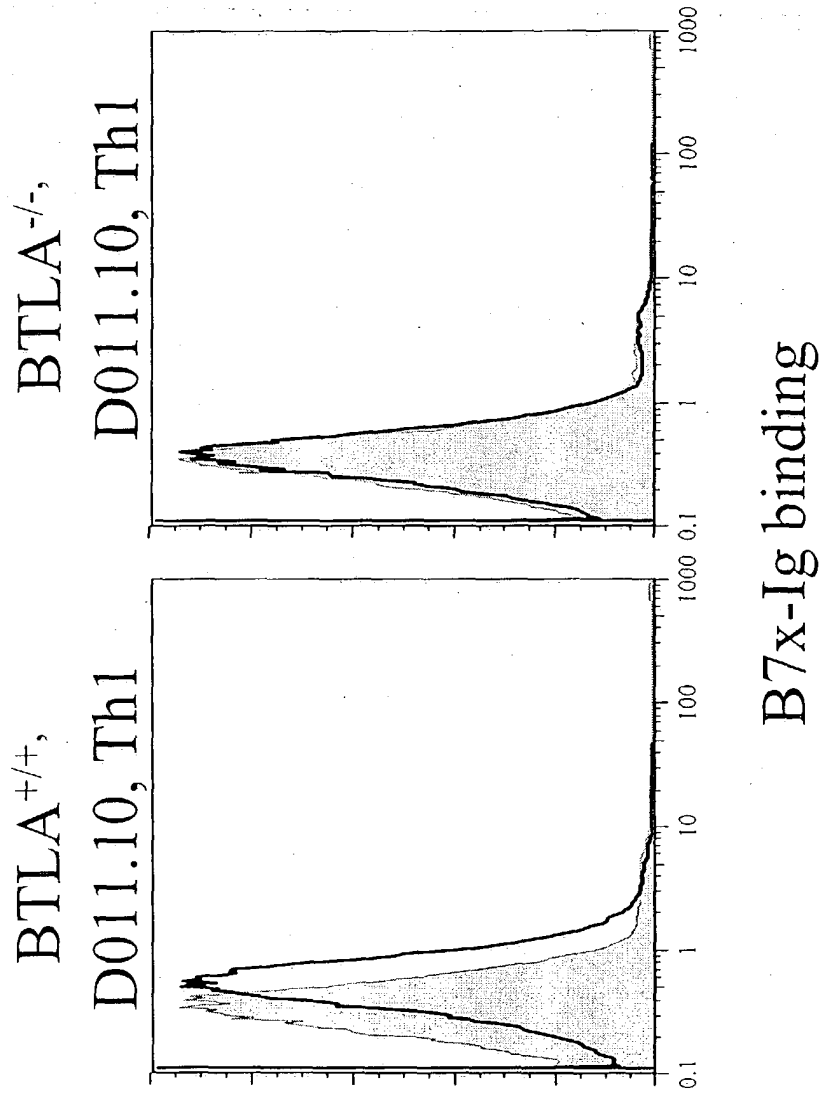


FIGURE 13B

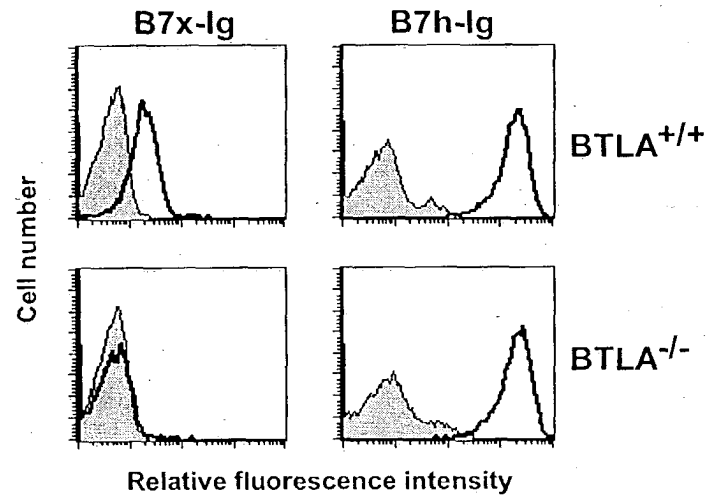


FIGURE 14

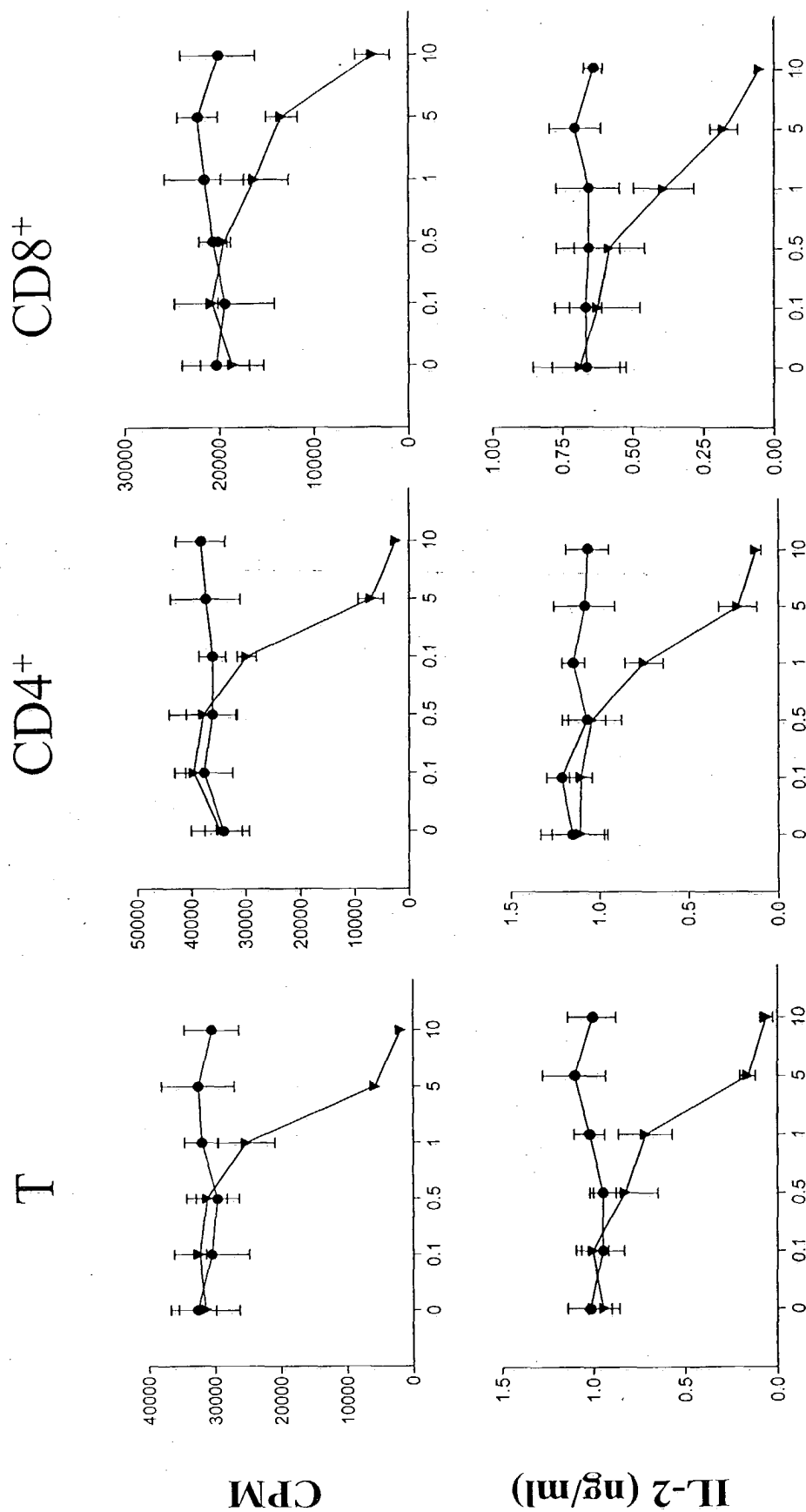


FIGURE 15

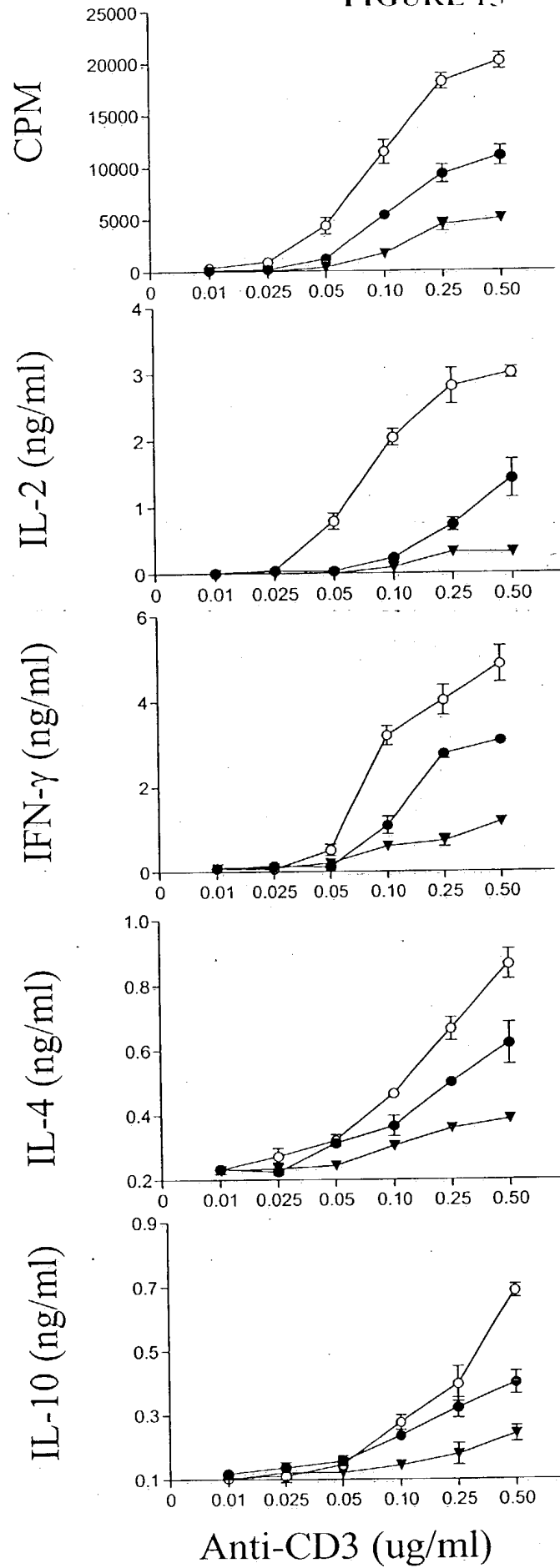
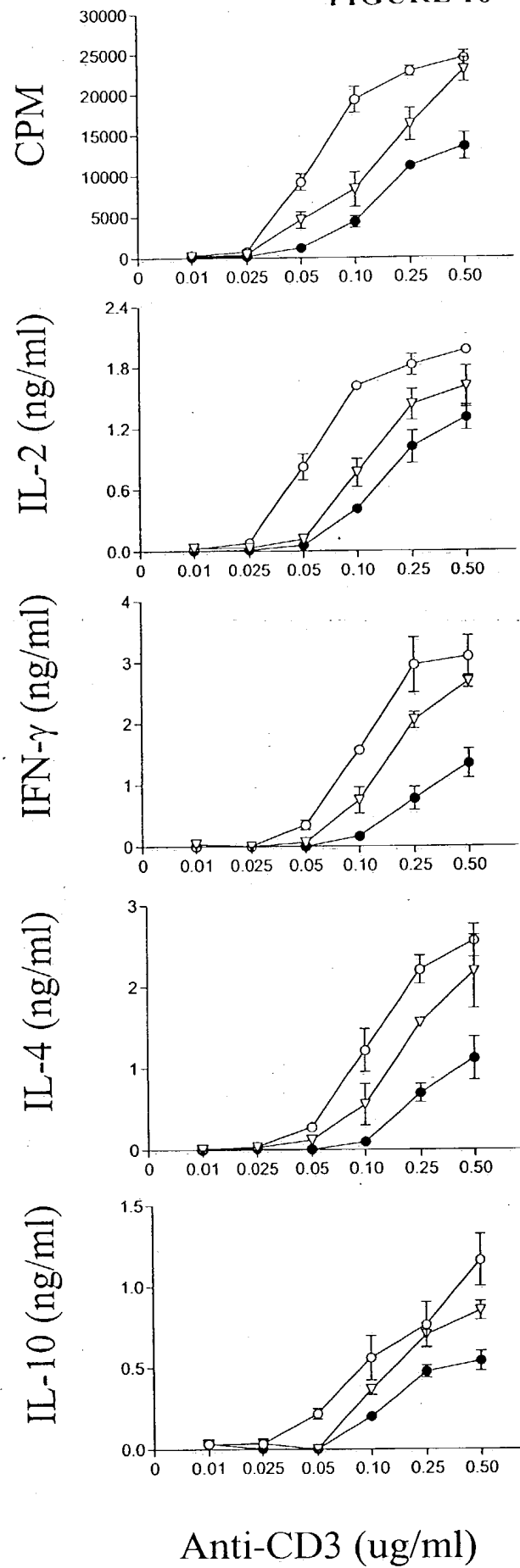
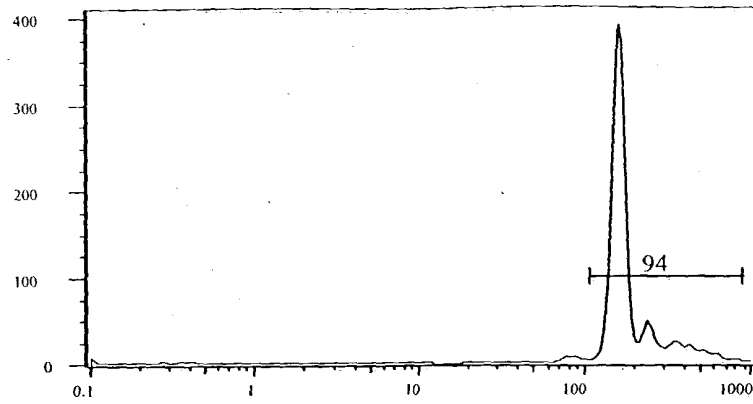




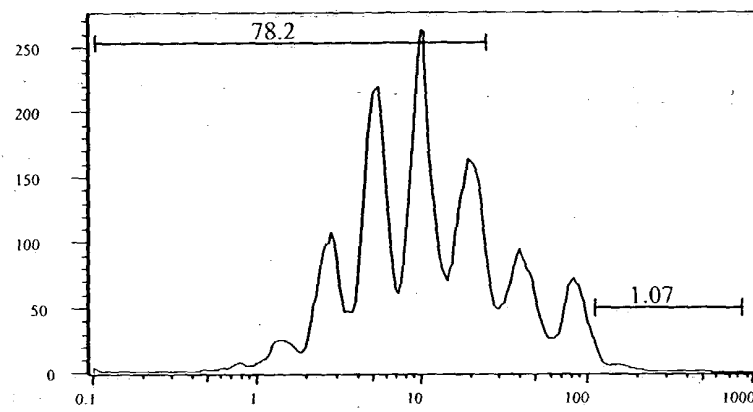
FIGURE 16



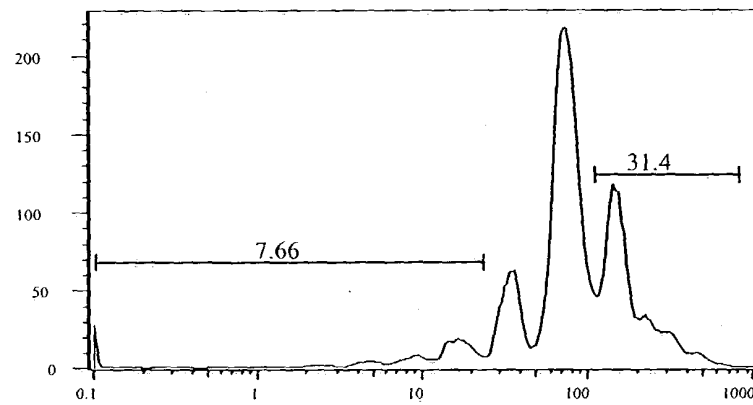
**FIGURE 17**



**GFP/CHO**

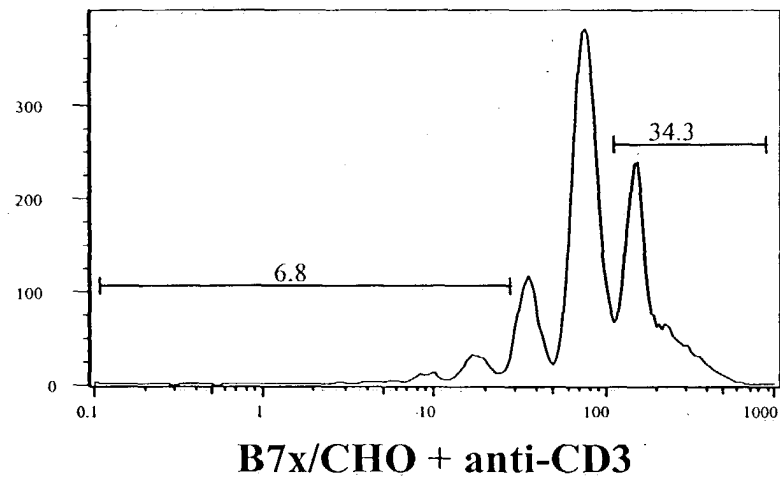
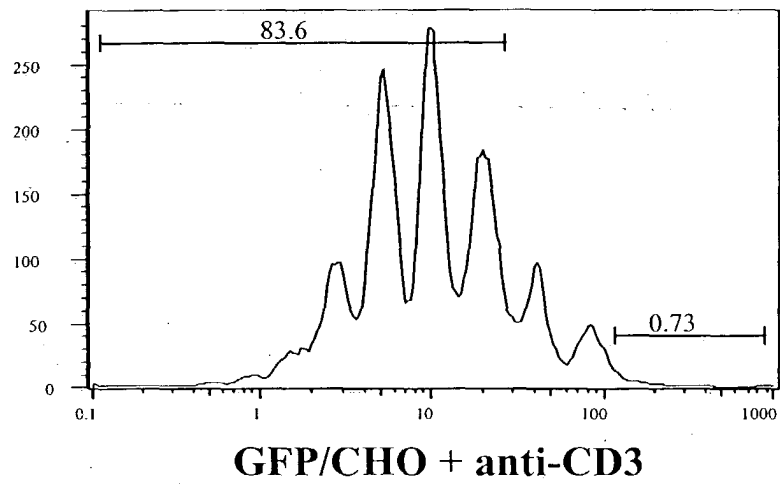
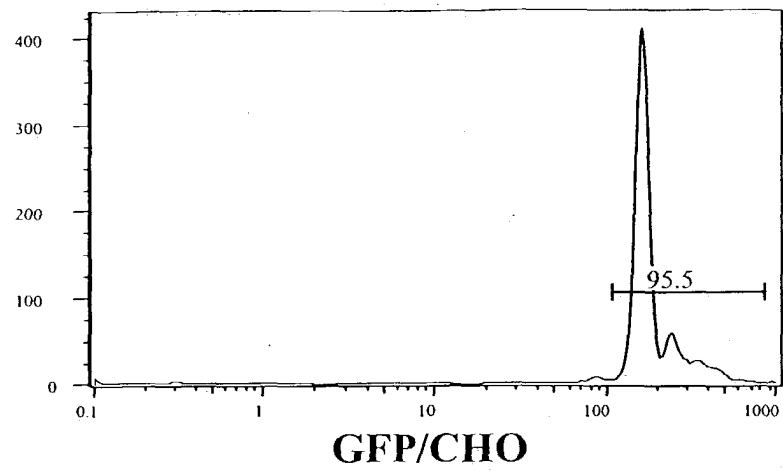


**GFP/CHO + anti-CD3**



**B7x/CHO + anti-CD3**

FIGURE 18



```

mouse BTLA 1 MKTVPAMLGTPRLFFREFFIL•HLGLWSILCEKATKRNDDEE
human BTLA MKTLPAMLGTTGKLFVWFFLIPYLDIWN.....HGKES

40 CEVQLNIKRNSKHS•AWT•GELFKIECPVKYCVHRPNVTWCK
CDVQ•LYIKRQSEHSILAGDPFELECPVKYCANRPHVTWCK

80 HNGTIWVPLEVGPQLYTSWEENRSVPVFLHFKPIHLSDN
LNGTTTCVKLEDR•Q•TSWKEEKNISFFILHFEPVLPNDN

120 GSYS•CSTNFNSQVINSHSVTIHVRERTQNSSEHPLITVSD
GSYRCSANFQSNLIESHSTTLYVTDVKSAS.....

160 IPDAT•NASGPSTMEERPGRTWLLYTLPLGALLLL•ACV
.....ERPSKDEMAS•RPWLLYSLLPLGGLPLLITTCF

199 CLLCFLKRIQGKEKKPSDLAGRDTNLVD.....IPASS
CLFCCLRRHQGKQNELSDTAGREINLVDAHLKSEQTEAST

232 RTNHQALPSC•TGIYDNDEPWSS•MQDESELTISLQSERNN
RQNSQVLLSE•TGIYDNDEPDLCFRMQEGSEVYSNPCLEENK

270 Q•GIVYASLNH•CVIGRNPRQENNMQ•EAPTEYASICVRS
EGIVYASLNH•SVIGLNSRLARNVKEAPTEYASICVRS

```

**FIGURE 20**

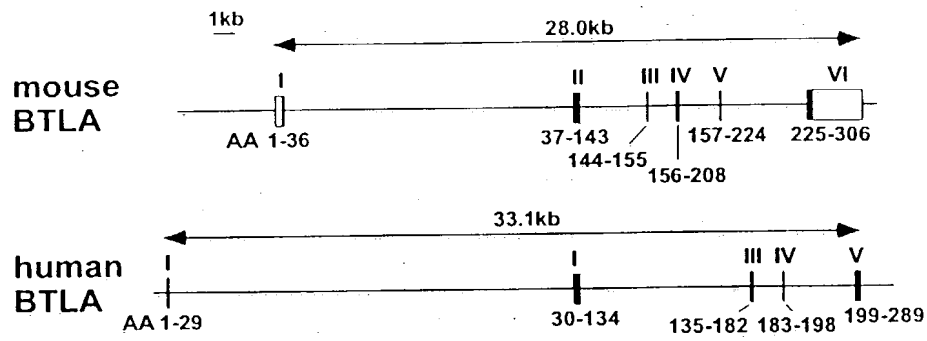
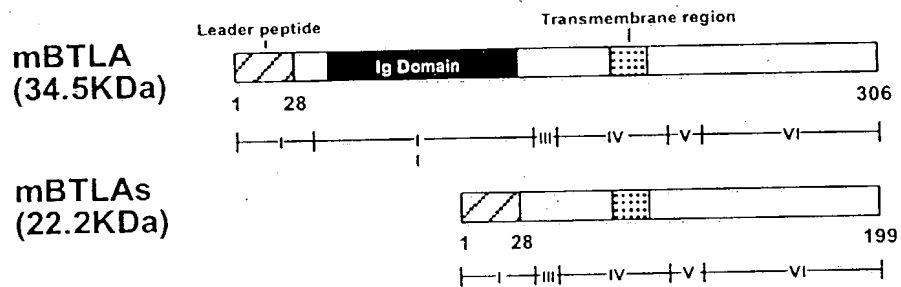


FIGURE 21



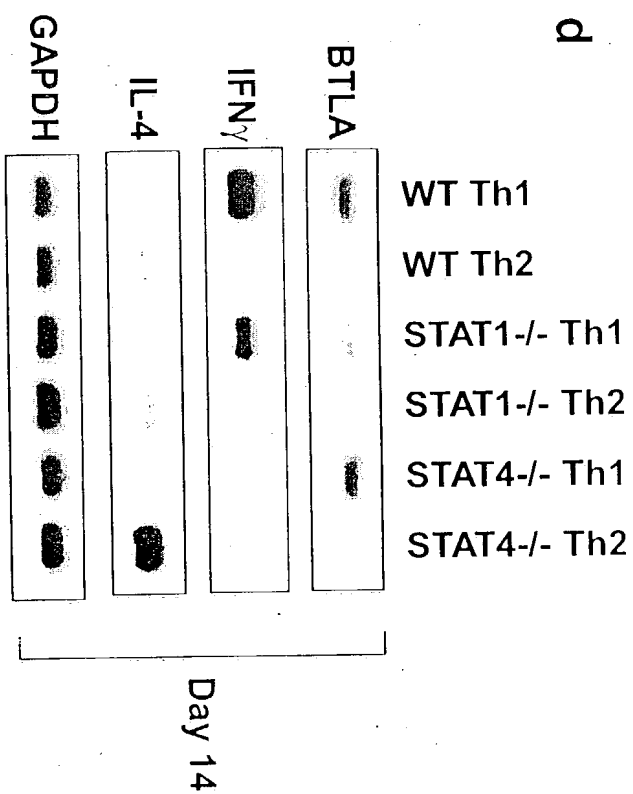
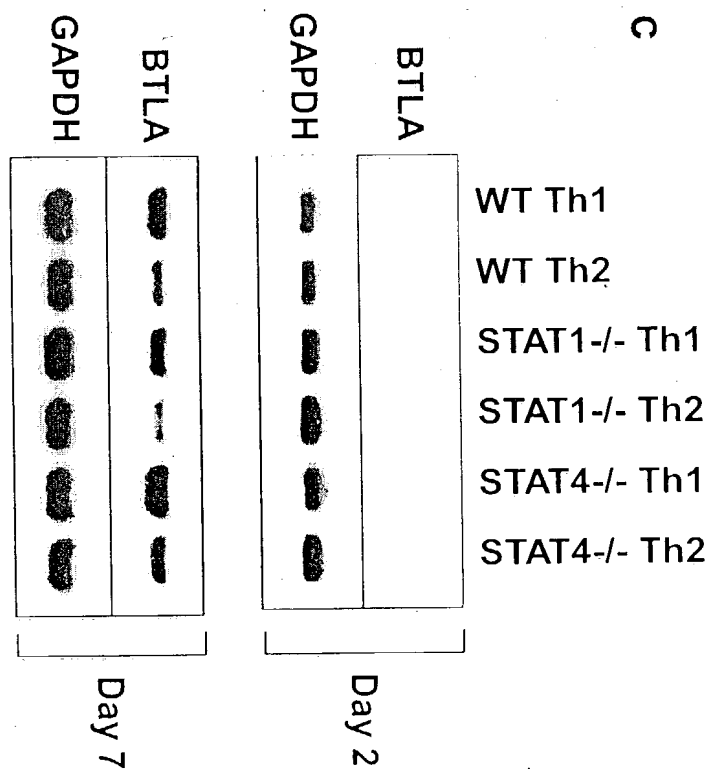
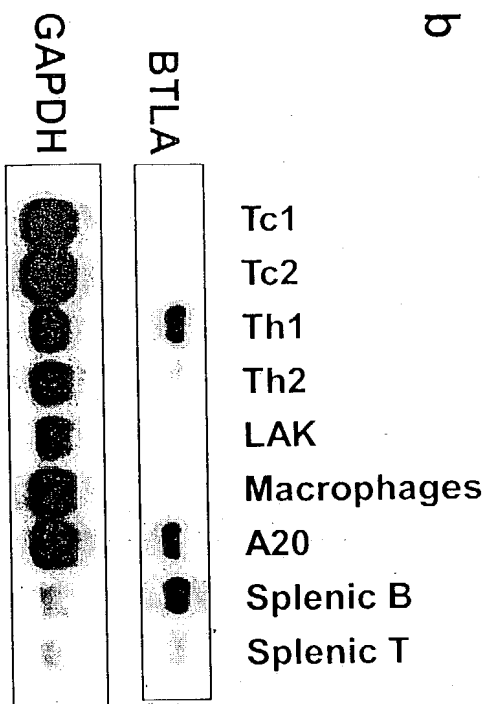
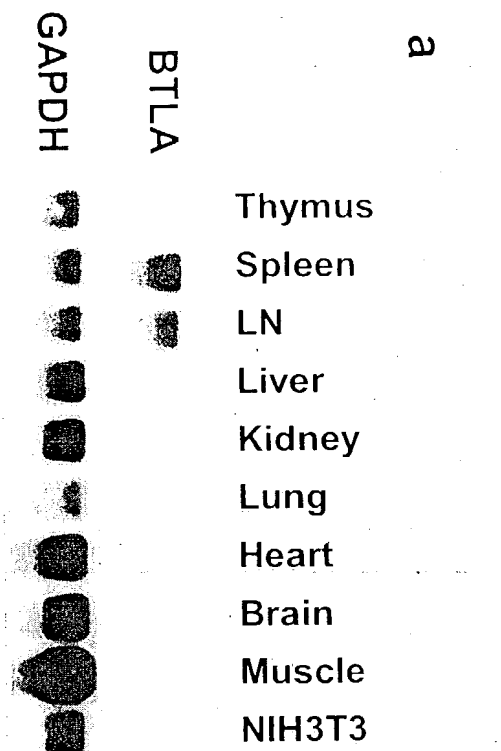
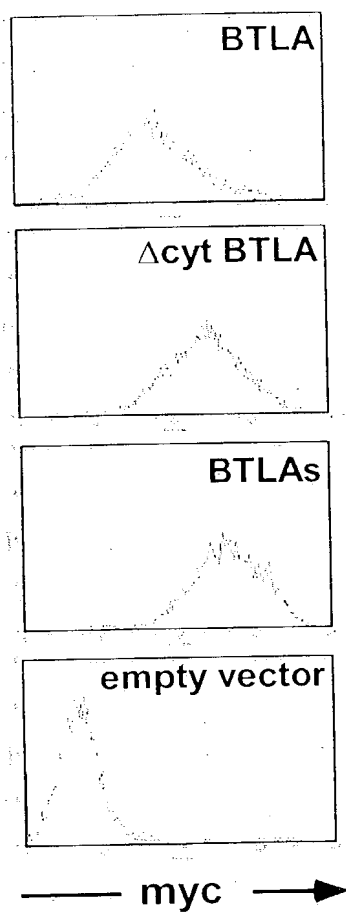
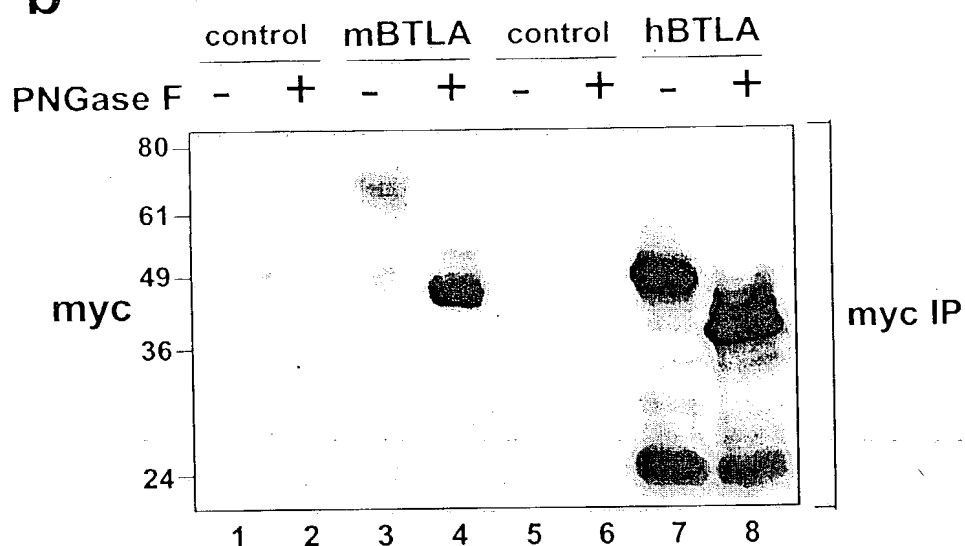
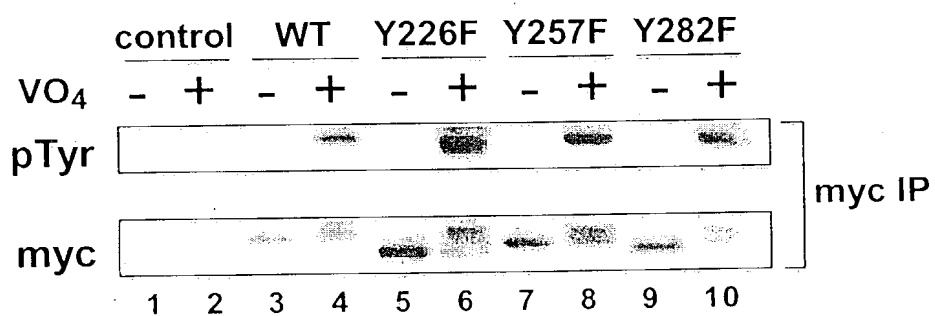
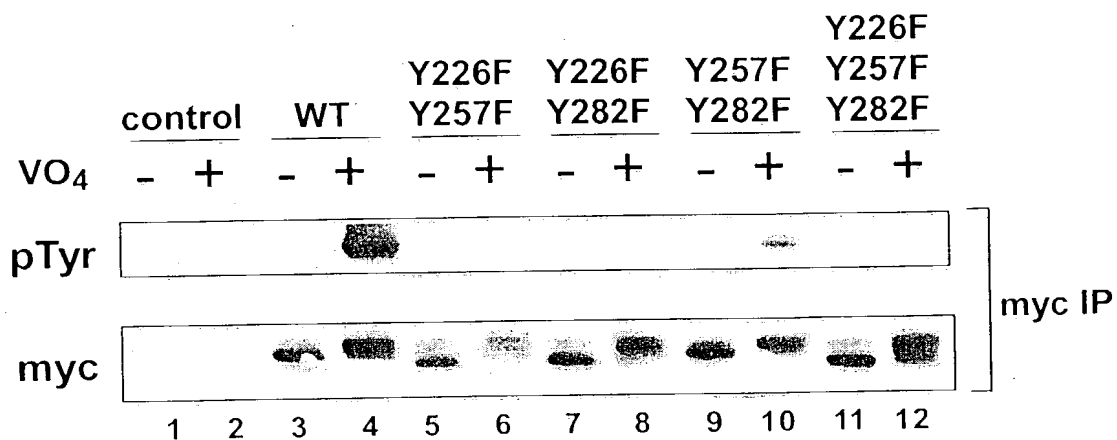


FIGURE 22

**a****b****c****d****FIGURE 23**



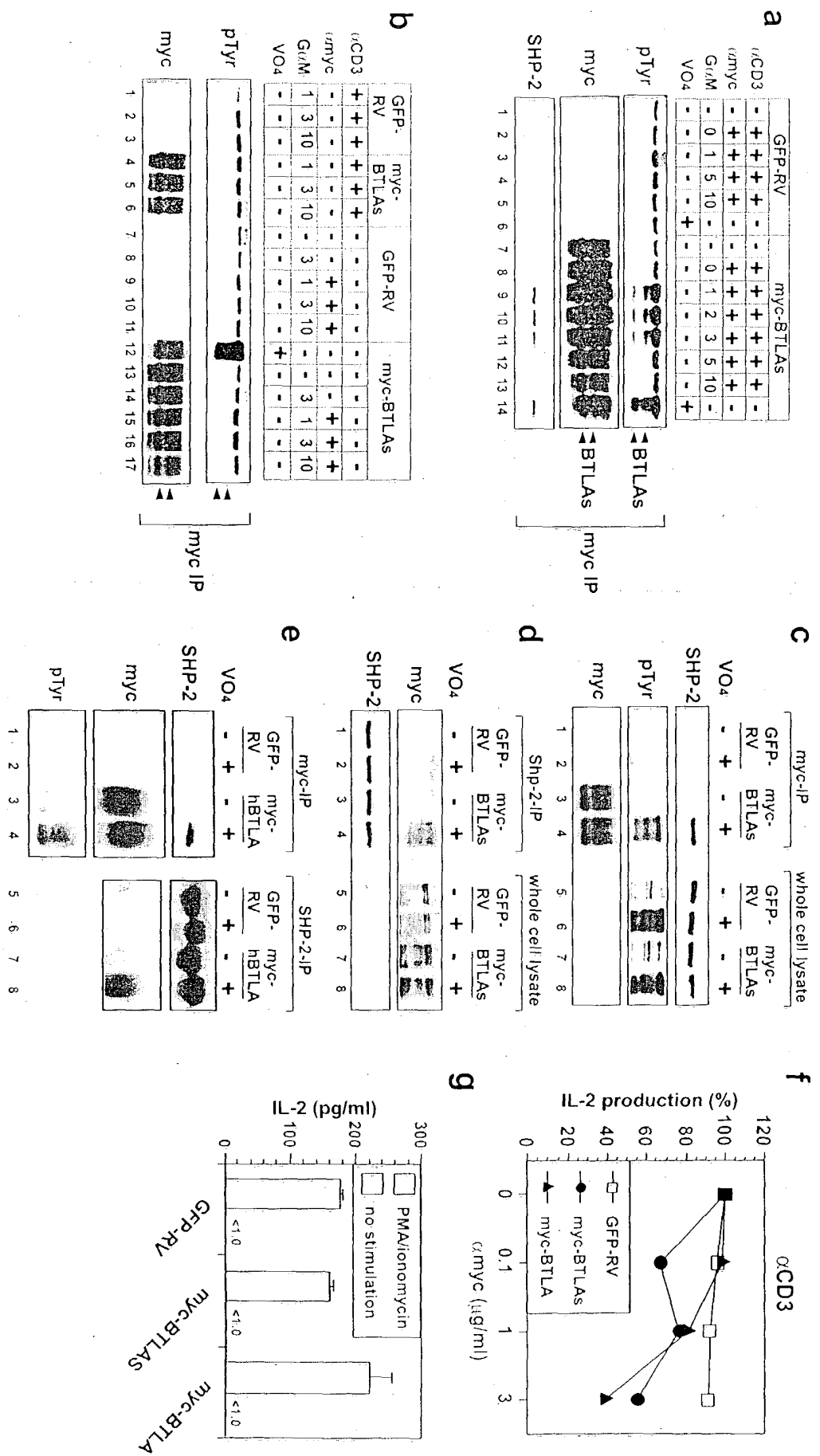


FIGURE 24

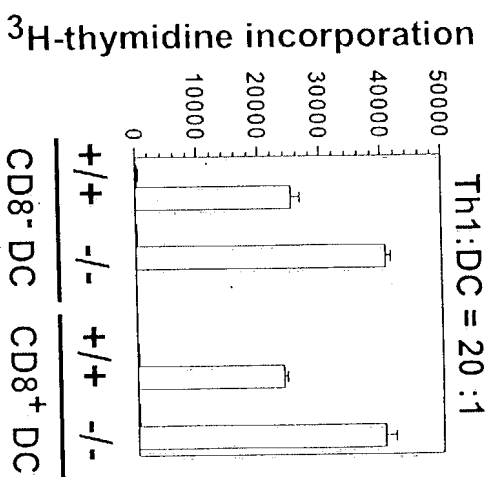
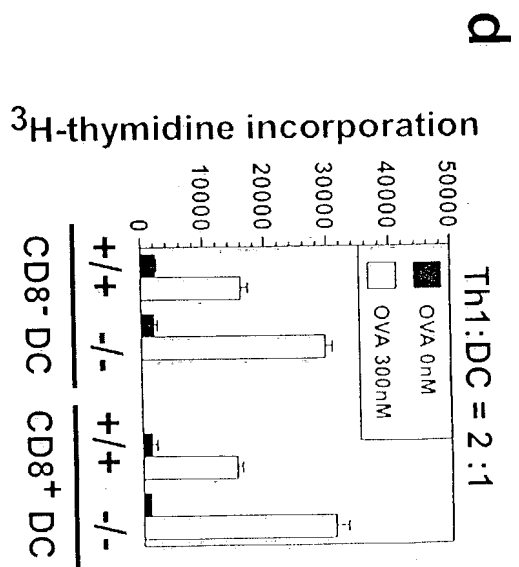
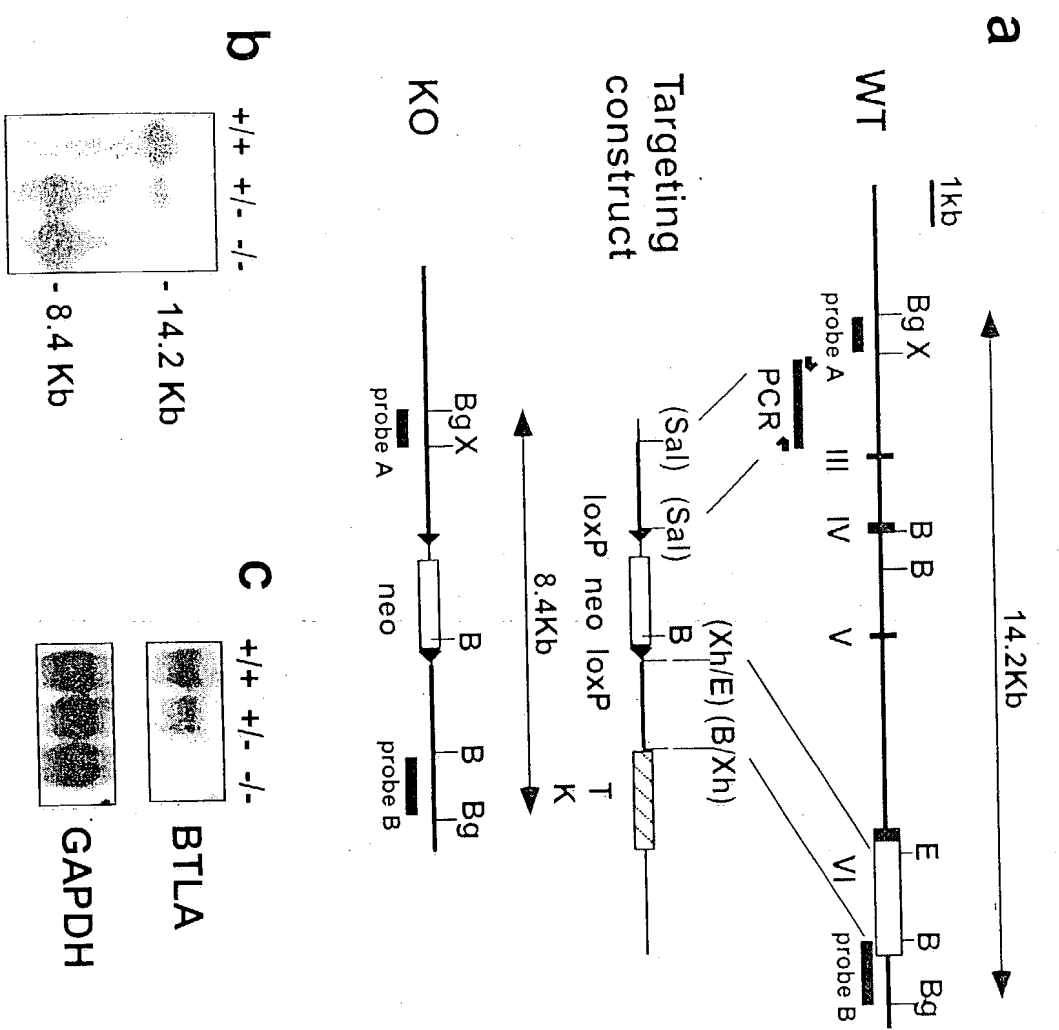


FIGURE 25

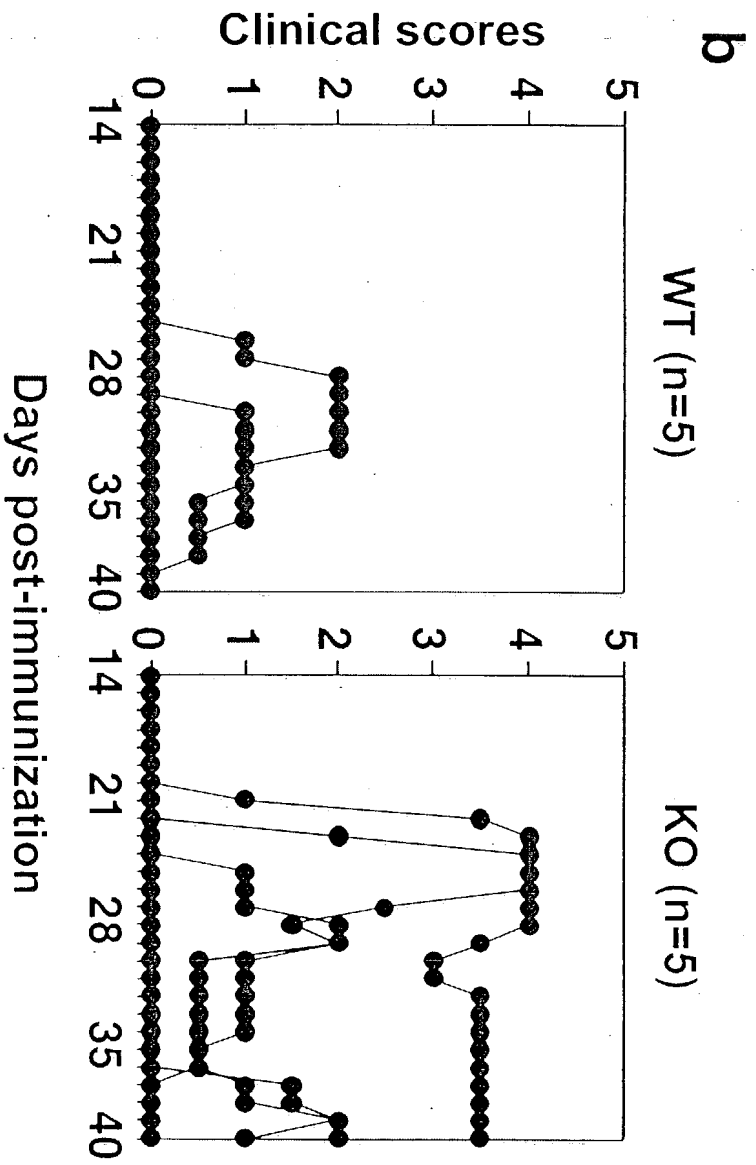
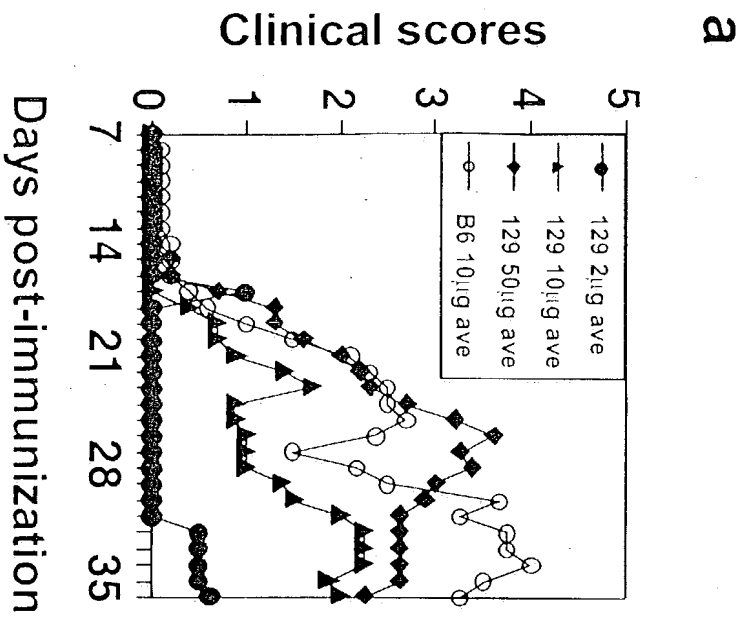


FIGURE 26

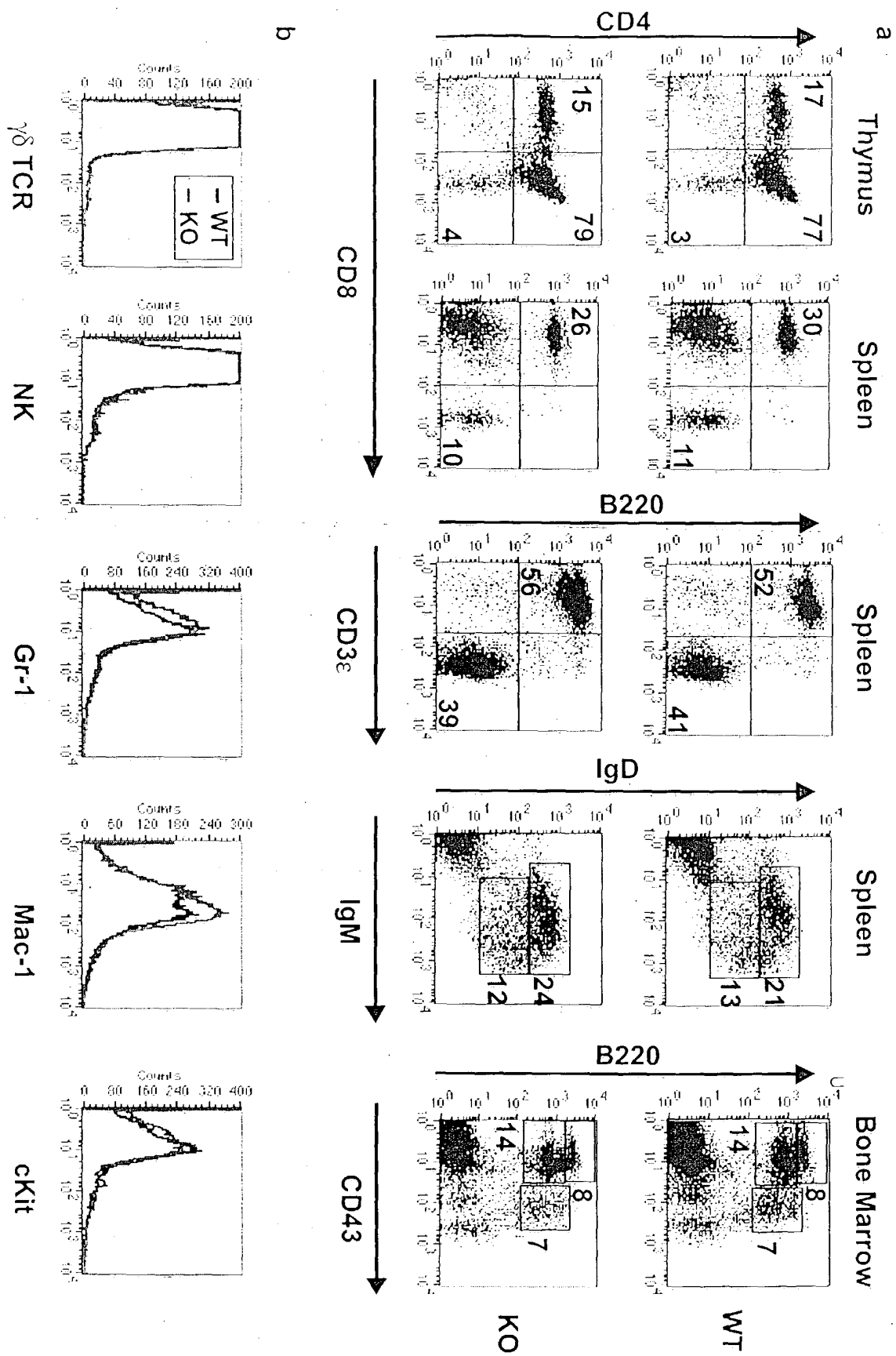


FIGURE 27

# HUMAN BTLA PROTEIN SEQUENCE

```

1   mktlpamlgt gklfwvffli pyldiwnihg kescdvqlii krgsehsila
51  gdpfelecpv kycanrphvt wcklngttcv kledrqtswk eeknisffil
101 hfepmlpndn gsyrcsanfg snlieshstt lyvtdvkgas erpskdevas
151 rpwllyslip lgglpllitt wfclfcclrr hqgkqnelsd tagreinlvd
201 ahlkseqtea strqnsqvll seagiydndp dlcfmqegs evcsnpclee
251 nkpgivyasl nhsviglinsr larnvkeapt eyasicvrs

```

# HUMAN BTLA NUCLEIC ACID SEQUENCE

```

1   atgaagacat tgccctgccat gcttgggaact gggaaattat tttgggtctt cttcttaatc
61  ccatatctgg acatctggaa catccatggg aaagaatcat gtgatgtaca gctttatata
121 aagagacaat ctgaacactc catcttagca ggagatccct ttgaactaga atgccctgtg
181 aaatactgtg ctaacaggcc tcatgtgact tggtgcaagc tcaatggaac aacatgtgta
241 aaacttgaag atagacaaac aagttggaag gaagagaaga acatttcatt tttcattcta
301 cattttgaac caatgcttcc taatgacaat gggtcatacc gctgttctgc aaattttcag
361 tctaattctc ttgaaagcca ctcaacaact ctttatgtga cagatgtaaa aggtgcctca
421 gaacgaccct ccaaggacga agtggcaagc agaccctggc tcctgtatag tttacttcct
481 ttgggggggat tgccctctact catcactacc tggttctgcc tgttctgetg cctgagaagg
541 caccaaggaa agcaaaatga actctctgac acagcaggaa gggaaattaa tctggttgat
601 gctcacctta agagcgagca aacagaagca agcaccaggc aaaattccca agtactgcta
661 tcagaagctg gaatttatga taatgacctt gacctttgtt tcaggatgca ggaagggctt
721 gaagtttggt ctaatccatg cctggaagaa aacaaaccag gcattgttta tgcttccttg
781 aaccattctg tcattggact gaactcaaga ctggcaagaa atgtaaaaga agcaccaaca
841 gaatatgcat ccatatgtgt gaggagttaa

```

FIGURE 28

# MOUSE BTLA PROTEIN SEQUENCE

```

1  mktvpamlgt prlfreffil hlglsilce katkrndeec evqlnikrns khsawtgelf
61  kiecpvkycv hrpnvtwckh ngtiwvplev gpqlytswee nrsvpvfvlh fkpihlndng
121 syscstnfns qvinshsvti hvrertqnss ehplitvsdi pdatnasgps tmeerpgrtw
181 llytllplga lllllacvel lcflkriqgk ekkpsdlagr dtnlvdipas srtnhqalps
241 gtgiydndpw ssmqdeselt islqsernnq givyaslnhc vigrnprqen nmqeapteya
301 sicvrs

```

# MOUSE BTLA NUCLEIC ACID SEQUENCE

```

1  atgaagacag tgccctgcat gcttgggact cctcggttat ttagggaatt cttcactctc
61  catctgggcc tctggagcat cctttgtgag aaagctacta agaggaatga tgaagagtgt
121 gaagtgcac ttaatattaa gaggaattcc aaacactctg cctggacagg agagtatttt
181 aaaattgaat gtccctgtgaa atactgtgtt catagacctt atgtgacttg gtgtaagcac
241 aatggaacaa tctgggtacc ccttgaagtt ggtcctcagc tatacactag ttgggaagaa
301 aatcgatcag ttccggtttt tgttctccat tttaaaccac tacatctcag tgataacggg
361 tcgtatagct gttctacaaa cttcaattct caagttatta atagccattc agtaaccate
421 catgtgagag aaaggactca aaactcttca gaacacccac taataacagt atctgacatc
481 ccagatgcca ccaatgcctc aggaccatcc accatggaag agaggccagg caggacttgg
541 ctgctttaca ccttgcttcc tttgggggca ttgcttctgc tccttgcttg tgtctgcttg
601 ctctgctttc tgaaaaggat ccaagggaaa gaaaagaagc cttctgactt ggcaggaagg
661 gacactaacc tggttgatat tccagccagt tccaggacaa atcaccaagc actgccatca
721 ggaactggaa tttatgataa tgatccctgg tctagcatgc aggatgaatc tgaattgaca
781 attagcttgc aatcagagag aaacaaccag ggcattgttt atgcttcttt gaaccattgt
841 gttattggaa ggaatccaag acaggaaaac aacatgcagg aggcacccac agaatatgca
901 tccatttgtg tgagaagtta a

```

FIGURE 29

## Section 1

	(1)	1	10	20	30	40	57
129 SvJ	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
MRL/lpr (bc)	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
C57Bl/6	(1)	GATGAAGAGTGTCCAGT	GCAACTTACTATTACGAGGAATTCCAAACAGTCTGCCAGG				
Balb/c	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
SWR	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
NZB/BinJ	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
NOD	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
MRL/lpr	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
DBA/2J	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
C3H/J	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
129SvEv	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
SJL.J	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
Celera old	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
WEHI 2 old	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
Bl/6 old	(1)	GATGAAGAGTGTCCAGT	GCAACTTACTATTACGAGGAATTCCAAACAGTCTGCCAGG				
WEHI 1old	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				
Consensus	(1)	GATGAAGAGTGTGAAGT	GCAACTTAATATTAAGAGGAATTCCAAACACTCTGCCTGG				

## Section 2

	(58)	58	70	80	90	100	114
129 SvJ	(58)	ACAGGAGAGTTATTTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTAAT				
MRL/lpr (bc)	(58)	ACAGGAGAGTTATTTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTCAT				
C57Bl/6	(58)	ACAGGAGAGTTATTTTAA	AATTCAATGTCCTGTGAAATACTGTGTTTCATAGACCTAAT				
Balb/c	(58)	ACAGGAGAGTTATTTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTAAT				
SWR	(58)	ACAGGAGAGTTATTTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTCAT				
NZB/BinJ	(58)	ACAGGAGAGTTATTTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTAAT				
NOD	(58)	ACAGGAGAGTTATTTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTAAT				
MRL/lpr	(58)	ACAGGAGAGTTATTTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTCAT				
DBA/2J	(58)	ACAGGAGAGTTATTTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTCAT				
C3H/J	(58)	ACAGGAGAGTTATTTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTAAT				
129SvEv	(58)	ACAGGAGAGTTATTTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTAAT				
SJL.J	(58)	ACAGGAGAGTTATTTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTAAT				
Celera old	(58)	ACAGGAGAGTTATTTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTAAT				
WEHI 2 old	(58)	ACAGGAGAGTTATTTTAA	AATTGAATGTCCTGTGGAATACTGTGTTTCATAGACCTCAT				
Bl/6 old	(58)	ACAGGAGAGTTATTTTAA	AATTCAATGTCCTGTGAAATACTGTGTTTCATAGACCTAAT				
WEHI 1old	(58)	ACAGGAGAGTTATTTTAA	AATTGAATGTCCTGTGGAATACTGTGTTTCATAGACCTCAT				
Consensus	(58)	ACAGGAGAGTTATTTTAA	AATTGAATGTCCTGTGAAATACTGTGTTTCATAGACCTAAT				

FIGURE 30

## Section 3

	(115)	115	120	130	140	150	160	171
129 SvJ (115)	GTGACTTGGT	GTAAGCACAAT	GGAACAATCT	GGGTACCCCTT	GAAAGTTGGT	CCCTCAG		
MRL/lpr (bc) (115)	GTGACTTGGT	GTAAGCACAAT	GGAACAATCT	GGGTACCCCTT	GAAAGTTGGT	CCCTCAG		
C57Bl/6 (115)	GTGACTTGGT	GTAAGCACAAT	GGAACAATCT	GGGTACCCCTT	GAAAGTTGGT	CCCTCAG		
Balb/c (115)	GTGACTTGGT	GTAAGCACAAT	GGAACAATCT	GGGTACCCCTT	GAAAGTTGGT	CCCTCAG		
SWR (115)	GTGACTTGGT	GTAAGCACAAT	GGAACAATCT	GGGTACCCCTT	GAAAGTTGGT	CCCTCAG		
NZB/BinJ (115)	GTGACTTGGT	GTAAGCACAAT	GGAACAATCT	GGGTACCCCTT	GAAAGTTGGT	CCCTCAG		
NOD (115)	GTGACTTGGT	GTAAGCACAAT	GGAACAATCT	GGGTACCCCTT	GAAAGTTGGT	CCCTCAG		
MRL/lpr (115)	GTGACTTGGT	GTAAGCACAAT	GGAACAATCT	GGGTACCCCTT	GAAAGTTGGT	CCCTCAG		
DBA/2J (115)	GTGACTTGGT	GTAAGCACAAT	GGAACAATCT	GGGTACCCCTT	GAAAGTTGGT	CCCTCAG		
C3H/J (115)	GTGACTTGGT	GTAAGCACAAT	GGAACAATCT	GGGTACCCCTT	GAAAGTTGGT	CCCTCAG		
129SvEv (115)	GTGACTTGGT	GTAAGCACAAT	GGAACAATCT	GGGTACCCCTT	GAAAGTTGGT	CCCTCAG		
SJL.J (115)	GTGACTTGGT	GTAAGCACAAT	GGAACAATCT	GGGTACCCCTT	GAAAGTTGGT	CCCTCAG		
Celera old (115)	GTGACTTGGT	GTAAGCACAAT	GGAACAATCT	GGGTACCCCTT	GAAAGTTGGT	CCCTCAG		
WEHI 2 old (115)	GTGACTTGGT	GTAAGCACAAT	GGAACAATCT	GGGTACCCCTT	GAAAGTTGGT	CCCTCAG		
Bl/6 old (115)	GTGACTTGGT	GTAAGCACAAT	GGAACAATCT	GGGTACCCCTT	GAAAGTTGGT	CCCTCAG		
WEHI 1old (115)	GTGACTTGGT	GTAAGCACAAT	GGAACAATCT	GGGTACCCCTT	GAAAGTTGGT	CCCTCAG		
Consensus (115)	GTGACTTGGT	GTAAGCACAAT	GGAACAATCT	GGGTACCCCTT	GAAAGTTGGT	CCCTCAG		

## Section 4

	(172)	172	180	190	200	210	228
129 SvJ (172)	CTATACACTAGTTGGGAAGAAAAT	CGATCAGTTCCGGT	TTTTGTTCTCCAT	TTTTAAA			
MRL/lpr (bc) (172)	CTATACACTAGTTGGGAAGAAAAT	CGATCAGTTCCGGT	TTTTGTTCTCCAT	TTTTAAA			
C57Bl/6 (172)	CTATACACTAGTTGGGAAGAAAAT	CAATCAGTTCCGGT	TTTTGTTCTCCAT	TTTTAAA			
Balb/c (172)	CTATACACTAGTTGGGAAGAAAAT	CGATCAGTTCCGGT	TTTTGTTCTCCAT	TTTTAAA			
SWR (172)	CTATACACTAGTTGGGAAGAAAAT	CGATCAGTTCCGGT	TTTTGTTCTCCAT	TTTTAAA			
NZB/BinJ (172)	CTATACACTAGTTGGGAAGAAAAT	CGATCAGTTCCGGT	TTTTGTTCTCCAT	TTTTAAA			
NOD (172)	CTATACACTAGTTGGGAAGAAAAT	CGATCAGTTCCGGT	TTTTGTTCTCCAT	TTTTAAA			
MRL/lpr (172)	CTATACACTAGTTGGGAAGAAAAT	CGATCAGTTCCGGT	TTTTGTTCTCCAT	TTTTAAA			
DBA/2J (172)	CTATACACTAGTTGGGAAGAAAAT	CGATCAGTTCCGGT	TTTTGTTCTCCAT	TTTTAAA			
C3H/J (172)	CTATACACTAGTTGGGAAGAAAAT	CGATCAGTTCCGGT	TTTTGTTCTCCAT	TTTTAAA			
129SvEv (172)	CTATACACTAGTTGGGAAGAAAAT	CGATCAGTTCCGGT	TTTTGTTCTCCAT	TTTTAAA			
SJL.J (172)	CTATACACTAGTTGGGAAGAAAAT	CGATCAGTTCCGGT	TTTTGTTCTCCAT	TTTTAAA			
Celera old (172)	CTATACACTAGTTGGGAAGAAAAT	CGATCAGTTCCGGT	TTTTGTTCTCCAT	TTTTAAA			
WEHI 2 old (172)	CTATACACTAGTTGGGAAGAAAAT	CGATCAGTTCCGGT	TTTTGTTCTCCAT	TTTTAAA			
Bl/6 old (172)	CTATACACTAGTTGGGAAGAAAAT	CAATCAGTTCCGGT	TTTTGTTCTCCAT	TTTTAAA			
WEHI 1old (172)	CTATACACTAGTTGGGAAGAAAAT	CGATCAGTTCCGGT	TTTTGTTCTCCAT	TTTTAAA			
Consensus (172)	CTATACACTAGTTGGGAAGAAAAT	CGATCAGTTCCGGT	TTTTGTTCTCCAT	TTTTAAA			

FIGURE 30



	(229) 229	240	250	260	270	285
129 SvJ (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
MRL/lpr (bc) (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
C57Bl/6 (229)	CCAATACATCTCAGTGATAATGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
Balb/c (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
SWR (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
NZB/BinJ (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
NOD (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
MRL/lpr (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
DBA/2J (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
C3H/J (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
129SvEv (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
SJL.J (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
Celera old (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
WEHI 2 old (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
Bl/6 old (229)	CCAATACATCTCAGTGATAATGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
WEHI 1old (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					
Consensus (229)	CCAATACATCTCAGTGATAACGGGTCGTATAGCTGTTCTACAAACTTCAATTCTCAA					

	(286) 286	300	310	322
129 SvJ (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
MRL/lpr (bc) (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
C57Bl/6 (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGACAG			
Balb/c (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
SWR (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
NZB/BinJ (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
NOD (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
MRL/lpr (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
DBA/2J (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
C3H/J (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
129SvEv (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
SJL.J (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
Celera old (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
WEHI 2 old (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
Bl/6 old (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGACAG			
WEHI 1old (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			
Consensus (286)	GTTATTAATAGCCATTTCAGTAACCATCCATGTGAGAG			

FIGURE 30

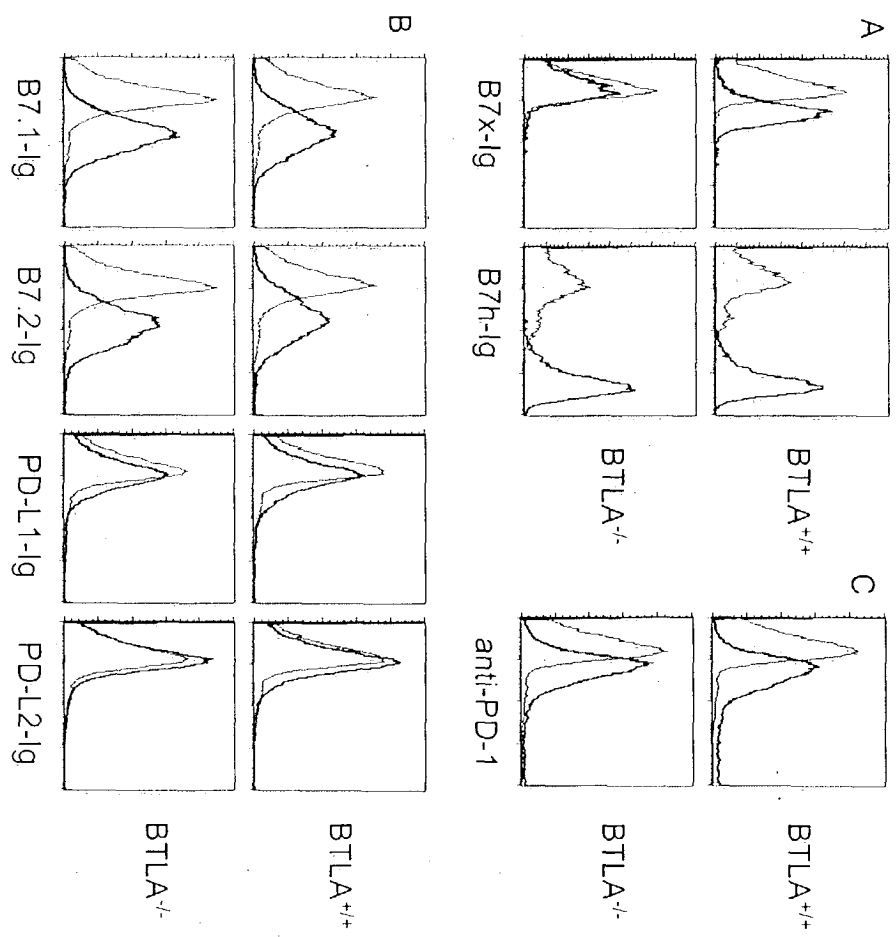
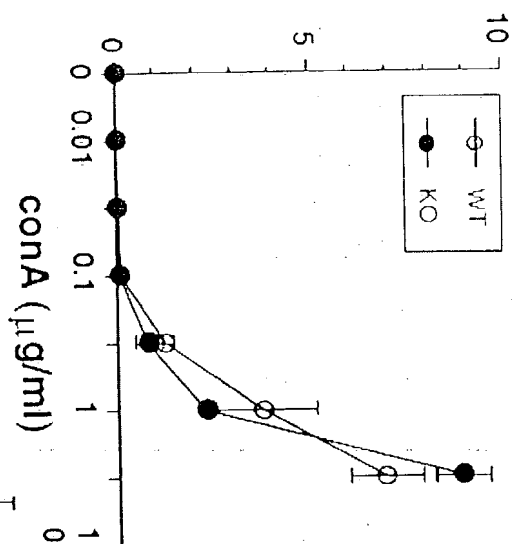


FIGURE 31

# T cells



# B cells

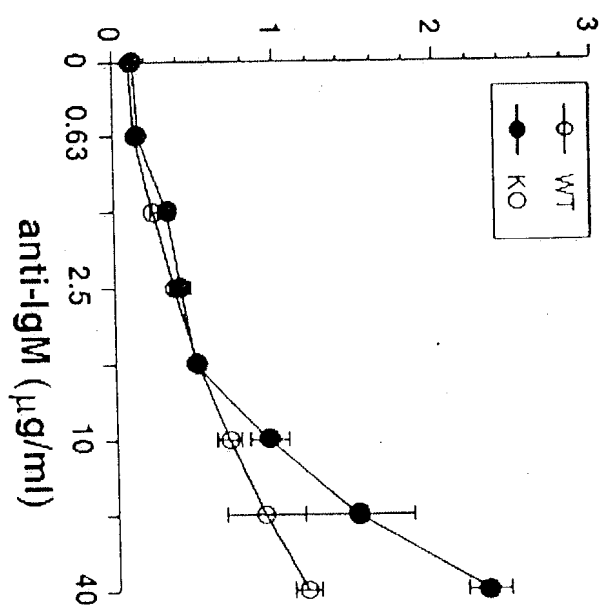
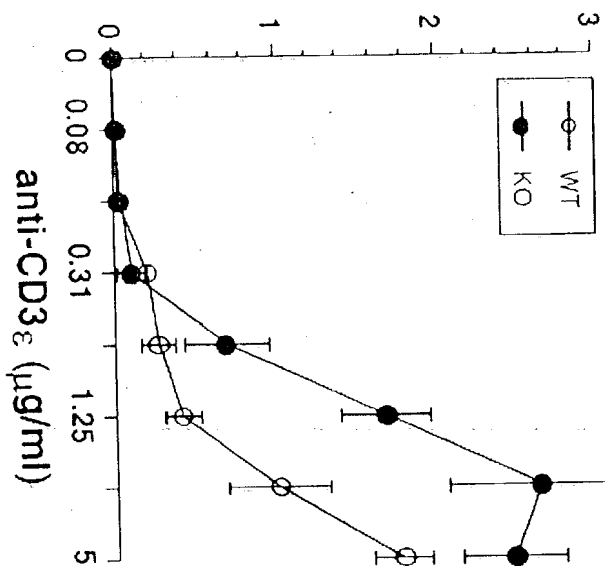
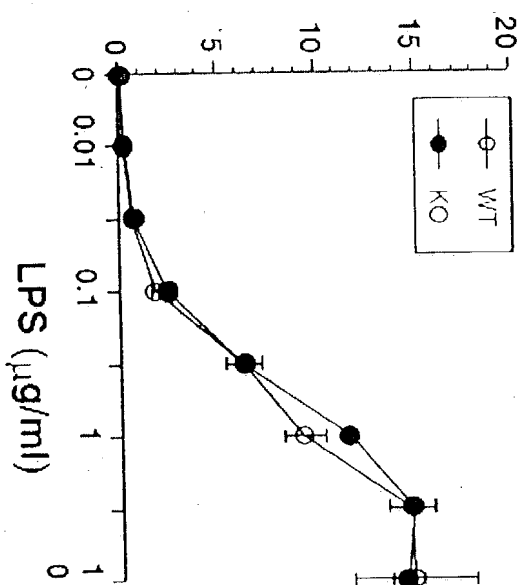


FIGURE 32